From:	Mertz, Prema
Sent:	Wednesday, October 12, 2005 1:30 PM
To:	STIC-Biotech/ChemLib
Subject:	10/666,225

Please search any 6 amino acids of SEQ ID NO:14 with protein databases.

Please search US PG PUB databases with SEQ ID NO:14.

Thanks.

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14-350aa
LB

10/14/05

****
Searcher:_____
Searcher Phone:_____
Date Searcher Picked up:_____
Date completed:_____
Searcher Prep Time:_____
Online Time:_____

****
Type of Search
NA#_____ AA#:_____
S/L:_____ Oligomer:_____
Encode/Transl:_____
Structure #:_____Text:____
Inventor:_____ Litigation:___

****
Vendors and cost where applicable
STN:_____
DIALOG:_____
QUESTEL/ORBIT:_____
LEXIS/NEXIS:_____
SEQUENCE SYSTEM:_____
WWW/Internet:_____
Other (Specify):_____

Date completed:	Search Site	Vendors
Searcher: _Beverly e 2528_	_____ STIC	_____ IG
Terminal time:	_____ CM-1	_____ STN
Elapsed time:	_____ Pre-S	_____ Dialog
CPU time:	Type of Search	_____ APS
Total time:	_____ N.A. Sequence	_____ Geninfo
Number of Searches:	_____ A.A. Sequence	_____ SDC
Number of Databases:	_____ Structure	_____ DARC/Questel
	_____ Bibliographic	__✓__ Other _CGN_

PTO-1590 (9-90)

OM protein - protein search, using sw model

GenCore version 5.1.6
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Run on: October 13, 2005, 18:35:50 ; Search time 42 Seconds
(without alignments)
801.806 Million cell updates/sec

Title: US-10-666-225-14
Perfect score: 350
Sequence: 1 MRLPDVQLWLVILWALVRAQ..........NGNVVKTDVPDMVVEACGCS 350

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 1748

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :
PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	67	19.1	350	2	JC5241	activin beta E cha
2	15	4.3	352	2	JC2466	inhibin beta-C cha
3	11	3.1	352	2	S70580	activin beta C pre
4	11	3.1	352	2	JC5366	activin beta C - m
5	9	2.6	151	2	S42296	bone morphogenetic
6	8	2.3	283	2	T14455	hypothetical prote
7	8	2.3	311	2	D86425	unknown protein [l
8	8	2.3	367	2	JC4151	activin beta D cha
9	8	2.3	480	2	S22701	mannosyltransferas
10	8	2.3	1045	2	A29840	serine proteinase
11	8	2.3	1060	2	S63993	acrosomal protein
12	8	2.3	1273	2	E72611	probable ATP-depen
13	8	2.0	72	2	S28793	major merozoite su
14	7	2.0	86	2	G84429	hypothetical prote
15	7	2.0	129	2	AH3212	hypothetical prote
16	7	2.0	130	2	F72513	hypothetical prote
17	7	2.0	135	2	H82641	hypothetical prote
18	7	2.0	169	2	C95394	protein [imported
19	7	2.0	183	2	H83561	hypothetical prote
20	7	2.0	184	2	B87708	hypothetical prote
21	7	2.0	189	2	B69005	probable 2-oxoglut
22	7	2.0	198	2	S48236	SNM1 protein - yea
23	7	2.0	233	2	A25814	glycoprotein 185 -
24	7	2.0	237	2	A4013	hypothetical prote
25	7	2.0	237	2	D40595	hypothetical prote
26	7	2.0	243	2	B96010	conserved hypothet
27	7	2.0	244	2	AF2753	transcription regu
28	7	2.0	245	2	S34242	hypothetical prote
29	7	2.0	247	2	G83798	ABC transporter (A
30	7	2.0	252	2	D97534	probable transcrip
31	7	2.0	274	2	A71275	hypothetical prote
32	7	2.0	281	2	B54498	major merozoite su
33	7	2.0	283	2	T36640	probable ABC-type
34	7	2.0	291	2	AF1722	post-translocation
35	7	2.0	292	2	T09784	homeobox leucine z
36	7	2.0	303	2	H75528	conserved hypothet
37	7	2.0	315	2	T10805	annexin - upland c
38	7	2.0	316	2	T31428	fiber annexin - up
39	7	2.0	334	2	T46885	3-methyl-2-oxobuta
40	7	2.0	334	2	T36511	probable branched-
41	7	2.0	338	2	AD3103	hypothetical prote
42	7	2.0	356	2	S16907	collagen alpha 1(I
43	7	2.0	362	2	H75398	probable succinyl-
44	7	2.0	371	2	B83781	hypothetical prote
45	7	2.0	378	2	AC1942	two-component sens
46	7	2.0	382	2	D75398	two-component resp
47	7	2.0	394	2	F69401	cell division prot
48	7	2.0	397	2	C82992	hypothetical prote
49	7	2.0	421	1	I64185	cell division prot
50	7	2.0	442	2	E72029	thiophene/furan ox
51	7	2.0	442	2	D86595	thiophene/furan ox
52	7	2.0	445	2	T47813	hypothetical prote
53	7	2.0	452	2	G70905	hypothetical prote
54	7	2.0	467	2	F64765	yaiU protein - Esc
55	7	2.0	471	2	AB3422	glutamyl-tRNA(gln)
56	7	2.0	474	2	D83396	conserved hypothet
57	7	2.0	495	2	B71311	probable thiophene
58	7	2.0	500	2	C64043	citrate (pro-3S)-1
59	7	2.0	506	2	T29968	hypothetical prote
60	7	2.0	546	2	D83408	hypothetical prote
61	7	2.0	581	2	C82043	hypothetical prote
62	7	2.0	588	2	T51154	probable transmemb
63	7	2.0	600	2	JC7725	mycodextranase (EC
64	7	2.0	602	2	G83388	probable binding p
65	7	2.0	652	2	T34497	hypothetical prote
66	7	2.0	668	2	AH0806	phosphoglycerate t
67	7	2.0	668	2	T11778	phosphoglycerate t
68	7	2.0	723	2	S70098	probable membrane
69	7	2.0	753	2	G70184	methyl-accepting c
70	7	2.0	763	2	A47563	glucose-6-phosphat
71	7	2.0	784	2	G95112	exoribonuclease, V
72	7	2.0	784	2	F97981	exoribonuclease R
73	7	2.0	804	2	T05783	hypothetical prote
74	7	2.0	848	2	B89042	protein F14F9.3 [1
75	7	2.0	872	2	T10582	hypothetical prote
76	7	2.0	889	1	S47162	DNA-directed RNA p
77	7	2.0	917	2	RDMDNH	nitrate reductase
78	7	2.0	941	2	C75633	ATP-dependent heli
79	7	2.0	962	1	SNECPI	pirilyin (EC 3.4.
80	7	2.0	962	2	H85533	pirilyin [Im
81	7	2.0	962	2	F91088	proteinase III [Im
82	7	2.0	968	2	T29532	hypothetical prote
83	7	2.0	974	2	T29007	translation elonga
84	7	2.0	1029	2	T30852	outer membrane pro
85	7	2.0	1039	2	T35878	hypothetical prote
86	7	2.0	1049	2	CGBC7S	fibronectin recept
87	7	2.0	1049	2	A27079	fibronectin recept
88	7	2.0	1058	2	A38564	ubiquitin-protein
89	7	2.0	1058	2	JC1254	ubiquitin-protein
90	7	2.0	1060	2	S06286	major merozoite su
91	7	2.0	1086	2	S16752	major merozoite su
92	7	2.0	1231	2	C84716	hypothetical prote
93	7	2.0	1487	2	EDBEE1	immediate-early pr
94	7	2.0	1487	2	EDBEF6	immediate-early pr
95	7	2.0	1488	2	AG2136	155K transcription
96	7	2.0	1631	1	SA2OK1	polyketide synthas
97	7	2.0	1639	2	S05603	major merozoite su
98	7	2.0	1640	2	A24594	major merozoite su
99	7	2.0	1669	1	CGH04B	probable major sur
100	7	2.0	1669	2	CGMS4B	collagen alpha 1(I
101	7	2.0	1701	2	A26868	collagen alpha 1(I
102	7	2.0	1701	2	A54498	major merozoite su

No.					Accession	Description
103	7	2.0	1708	2	F69189	protoporphyrin IX
104	7	2.0	1726	1	SAZQGM	major merozoite su
105	7	2.0	1726	2	A45548	major merozoite su
106	7	2.0	1894	2	C54689	protein-tyrosine-p
107	7	2.0	2021	2	A97859	190-kDa cell surfa
108	7	2.0	2249	2	A41477	190K surface antig
109	7	2.0	3169	2	T00296	toxin B - Escheric
110	7	2.0	3762	2	S75251	hypothetical prote
111	7	2.0	3972	2	B26762	protamine (mugilin
112	7	1.7	33	2	TYTUY2	protamine Y2 - blu
113	6	1.7	34	1	E87352	hypothetical prote
114	6	1.7	57	2	S18336	hypothetical prote
115	6	1.7	61	2	A38226	hypothetical prote
116	6	1.7	67	2	D72428	cAMP-dependent pro
117	6	1.7	68	2	E69871	hypothetical prote
118	6	1.7	69	2	F97551	hypothetical prote
119	6	1.7	74	2	D84003	hypothetical prote
120	6	1.7	74	2	D72269	hypothetical prote
121	6	1.7	74	2	H83765	hypothetical prote
122	6	1.7	75	2	I45885	conserved hypothet
123	6	1.7	76	2	JC1136	elastin - bovine (
124	6	1.7	76	2	B71840	hypothetical prote
125	6	1.7	76	2	B64675	conserved hypothet
126	6	1.7	80	2	G95414	probable bacteriop
127	6	1.7	86	2	AD0621	hypothetical prote
128	6	1.7	88	2	E87415	hypothetical prote
129	6	1.7	88	2	S77426	conserved hypothet
130	6	1.7	89	2	S55624	hypothetical prote
131	6	1.7	92	2	AG2795	major allergen cha
132	6	1.7	92	2	G97574	major allergen Fel
133	6	1.7	95	2	T10870	macrophage antibio
134	6	1.7	95	1	WTRBM2	defensin CS-4 prec
135	6	1.7	95	1	WTRBM1	hypothetical prote
136	6	1.7	96	2	S73274	hypothetical prote
137	6	1.7	96	2	S55624	conserved hypothet
138	6	1.7	96	2	AG2795	hypothetical 11.0K
139	6	1.7	97	2	G97574	y4kP protein - Rhi
140	6	1.7	99	2	AC0034	probable type III
141	6	1.7	99	2	T17020	auxin-induced prot
142	6	1.7	101	2	AI2695	hypothetical prote
143	6	1.7	102	2	E72533	hypothetical prote
144	6	1.7	103	2	PH1077	Ig light chain V r
145	6	1.7	103	2	C64308	hypothetical prote
146	6	1.7	105	2	T24311	hypothetical prote
147	6	1.7	105	2	JC5414	cortistatin-like p
148	6	1.7	105	2	S75861	hypothetical prote
149	6	1.7	105	2	S37489	ribosomal protein
150	6	1.7	105	2	AI2347	30S ribosomal prot
151	6	1.7	106	2	S70134	probable membrane
152	6	1.7	109	2	D69447	hypothetical prote
153	6	1.7	109	2	E72476	hypothetical prote
154	6	1.7	109	1	L77RB	Ig lambda chain C
155	6	1.7	110	2	T48748	hypothetical prote
156	6	1.7	111	2	AG0673	probable glutaredo
157	6	1.7	112	2	B28302	probable secreted
158	6	1.7	113	2	T12779	beta-galactoside-b
159	6	1.7	114	2	G98105	neurofilament-L su
160	6	1.7	114	2	A46024	transcription regu
161	6	1.7	114	2	S26278	T cell receptor be
162	6	1.7	115	2	S17380	T-cell receptor be
163	6	1.7	115	2	S48982	hypothetical prote
164	6	1.7	115	2	PN0504	activin beta A cha
165	6	1.7	116	2	D33932	Ig mu chain precur
166	6	1.7	116	2	D75507	hypothetical prote
167	6	1.7	116	2	HVMS31	Ig heavy chain pre
168	6	1.7	116	2	RGECMD	modulator protein
169	6	1.7	117	2	A75111	hypothetical prote
170	6	1.7	117	1	HVCQE1	Ig heavy chain pre
171	6	1.7	118	2	B30505	Ig lambda-6 chain
172	6	1.7	118	2	A30505	Ig lambda chain C
173	6	1.7	118	2	T35585	hypothetical prote
174	6	1.7	119	2	E70161	ribosomal protein
175	6	1.7	119	2	S45992	probable membrane

No.					Accession	Description
176	6	1.7	120	2	S30770	ribosomal protein
177	6	1.7	120	2	B97067	uncharacterized pr
178	6	1.7	121	2	G97833	hypothetical prote
179	6	1.7	121	2	S64508	hypothetical prote
180	6	1.7	122	2	F72636	hypothetical prote
181	6	1.7	123	2	S63055	probable membrane
182	6	1.7	124	2	C83137	probable membrane
183	6	1.7	125	2	E83746	hypothetical prote
184	6	1.7	125	2	S43295	PTS system, glucit
185	6	1.7	129	2	S03342	bone morphogenetic
186	6	1.7	129	2	AH2003	DNA-directed RNA p
187	6	1.7	129	2	G70667	hypothetical prote
188	6	1.7	133	2	AB3465	hypothetical prote
189	6	1.7	134	2	B87022	hypothetical prote
190	6	1.7	135	2	LNHUGB	probable ribosomal
191	6	1.7	136	2	S07637	Ig heavy chain pre
192	6	1.7	136	2	D64324	ribosomal protein
193	6	1.7	137	2	AVM335	Ig heavy chain pre
194	6	1.7	138	2	T45371	probable ribosomal
195	6	1.7	138	2	G70642	galectin 1 [valida
196	6	1.7	139	2	H87362	organic hydroperox
197	6	1.7	139	2	AF0685	conserved hypothet
198	6	1.7	139	2	AB0110	transcription regu
199	6	1.7	139	2	PC4217	conserved hypothet
200	6	1.7	140	2	D95896	hypothetical prote
201	6	1.7	140	2	S14179	conserved hypothet
202	6	1.7	140	2	S04165	conserved hypothet
203	6	1.7	140	2	C69080	hypothetical prote
204	6	1.7	141	2	T36136	organic hydroperox
205	6	1.7	141	2	AB0110	conserved hypothet
206	6	1.7	142	2	B72688	transcription regu
207	6	1.7	142	2	B92241	conserved hypothet
208	6	1.7	143	1	A87653	CheZ protein [impo
209	6	1.7	145	2	GDBY	glutaredoxin - yea
210	6	1.7	145	2	S32213	NTP pyrophosphohyd
211	6	1.7	145	2	AI2869	transcription regu
212	6	1.7	145	2	AI3048	probable regulator
213	6	1.7	146	2	B98237	hypothetical prote
214	6	1.7	146	2	T36476	conserved hypothet
215	6	1.7	147	2	H75394	conserved hypothet
216	6	1.7	147	2	C97646	hypothetical prote
217	6	1.7	150	2	D71540	hypothetical prote
218	6	1.7	150	2	I59431	PR310 c-K-ras onco
219	6	1.7	151	2	T34697	probable insertion
220	6	1.7	151	2	E83550	positive regulator
221	6	1.7	152	2	AE1929	hypothetical prote
222	6	1.7	153	2	A71682	hypothetical prote
223	6	1.7	153	2	T47392	hypothetical prote
224	6	1.7	153	2	F71902	xanthine-guanine p
225	6	1.7	153	2	T54498	hypothetical prote
226	6	1.7	155	2	S28699	hypothetical prote
227	6	1.7	155	2	P87696	hypothetical prote
228	6	1.7	156	2	B85814	hypothetical prote
229	6	1.7	156	2	B90966	DNA mismatch endon
230	6	1.7	156	2	JS0264	DNA mismatch endon
231	6	1.7	157	2	S35538	DNA mismatch endon
232	6	1.7	157	2	D82209	probable antioxida
233	6	1.7	157	2	B69221	E6 protein - human
234	6	1.7	158	2	AI2382	conserved hypothet
235	6	1.7	159	2	S57630	hypothetical prote
236	6	1.7	160	2	T17000	hypothetical prote
237	6	1.7	160	1	A35261	Alginate regulator
238	6	1.7	161	1	HMECA1	hemagglutinin AFA-
239	6	1.7	161	2	T04981	hypothetical prote
240	6	1.7	163	2	A70847	hypothetical prote
241	6	1.7	164	2	AB3299	phosphinothricin N
242	6	1.7	164	2	AE3299	protein-tyrosine-p
243	6	1.7	164	2	T37174	hypothetical prote
244	6	1.7	165	2	F72470	probable insertion
245	6	1.7	165	2	T36981	probable periplasm
246	6	1.7	167	2	A92046	ultra high-sulfur
247	6	1.7	169	2	A12090	hypothetical prote
248	6	1.7	169	2	S18946	hypothetical prote

249	6	1.7	170	2	T22473	hypothetical prote
250	6	1.7	170	2	S39880	hypothetical prote
251	6	1.7	171	2	AH3310	ribosomal RNA meth
252	6	1.7	172	2	T08650	hypothetical prote
253	6	1.7	173	1	RKDWS	ribulose-bisphosph
254	6	1.7	174	2	G72381	hypothetical prote
255	6	1.7	175	2	AB0428	hypothetical prote
256	6	1.7	176	1	PWEC	inorganic diphosph
257	6	1.7	176	2	D86120	inorganic diphosph
258	6	1.7	176	2	D91279	inorganic pyrophos
259	6	1.7	176	2	S12914	inorganic pyrophos
260	6	1.7	176	2	T35459	hypothetical prote
261	6	1.7	178	2	C86824	calponin - turkey
262	6	1.7	178	2	B69864	hypothetical prote
263	6	1.7	178	1	C87553	probable methionin
264	6	1.7	178	2	A99314	hypothetical prote
265	6	1.7	182	1	R5MX6	hypothetical prote
266	6	1.7	182	2	A36686	ribosomal protein
267	6	1.7	182	2	G75538	ultra-high-sulfur
268	6	1.7	183	2	S53143	conserved hypothet
269	6	1.7	183	2	T07241	core antigen - hep
270	6	1.7	183	2	T47707	hypothetical prote
271	6	1.7	184	2	T30611	hypothetical prote
272	6	1.7	184	2	AB1876	hypothetical prote
273	6	1.7	184	2	AD2363	hypothetical prote
274	6	1.7	185	2	T14523	hypothetical prote
275	6	1.7	185	2	T15580	hypothetical prote
276	6	1.7	185	2	C89883	conserved hypothet
277	6	1.7	186	2	F82046	proteinase H8lVU,
278	6	1.7	186	2	E87433	conserved hypothet
279	6	1.7	187	2	S09554	transforming prote
280	6	1.7	187	2	C75136	hypothetical prote
281	6	1.7	187	2	AE3442	hypothetical prote
282	6	1.7	189	2	A99217	cytidylate kinase
283	6	1.7	190	2	P97008	hypothetical prote
284	6	1.7	191	2	I46412	keratin KAP5.4 - s
285	6	1.7	191	2	E84426	keratin KAP5.5 - s
286	6	1.7	191	2	T26391	hypothetical prote
287	6	1.7	194	2	A84495	ycf4 protein - Chl
288	6	1.7	196	2	JQ1078	hypothetical prote
289	6	1.7	196	2	B70827	stylar glycoprotei
290	6	1.7	196	2	D90646	hypothetical prote
291	6	1.7	196	2	D85497	probable fimbrial
292	6	1.7	196	2	I46413	probable fimbrial
293	6	1.7	197	2	T07995	transcription regu
294	6	1.7	197	1	T47159	hypothetical prote
295	6	1.7	197	2	A83845	hypothetical prote
296	6	1.7	197	2	AB2162	hypothetical prote
297	6	1.7	197	2	G82973	hypothetical prote
298	6	1.7	198	1	E71461	transcription regu
299	6	1.7	199	2	VCVQB3	coat protein - bar
300	6	1.7	199	2	S10986	coat protein - bar
301	6	1.7	200	2	T36125	hypothetical prote
302	6	1.7	200	2	T40548	hypothetical prote
303	6	1.7	201	2	A64677	orotate phosphorib
304	6	1.7	201	2	G71837	orotate phosphorib
305	6	1.7	202	2	F70690	hypothetical prote
306	6	1.7	203	2	D82018	hypothetical prote
307	6	1.7	203	2	G81000	conserved hypothet
308	6	1.7	206	2	T36643	probable integral
309	6	1.7	207	2	E69085	conserved hypothet
310	6	1.7	208	2	B95223	conserved hypothet
311	6	1.7	208	2	D98087	conserved hypothet
312	6	1.7	208	2	B87281	glutathione S-tran
313	6	1.7	209	2	S48024	dnaK-type molecula
314	6	1.7	209	2	F82483	dnaK-type molecula
315	6	1.7	210	2	S48025	hypothetical prote
316	6	1.7	210	2	S36297	T-cell receptor ga
317	6	1.7	210	2	S48023	dnaK-type molecula
318	6	1.7	211	2	T21120	hypothetical prote
319	6	1.7	211	2	B70648	probable nuol prot
320	6	1.7	212	2	C75330	thymidine kinase (
321	6	1.7	212	2	H82389	glutaredoxin-relat

322	6	1.7	214	2	A03309	dnaK-type molecula
323	6	1.7	214	2	A82738	transcription regu
324	6	1.7	215	2	S62823	adenylate kinase (
325	6	1.7	215	2	S78275	ribosomal protein
326	6	1.7	216	2	T47681	hypothetical prote
327	6	1.7	216	2	T05359	hypothetical prote
328	6	1.7	217	2	AD2568	hypothetical prote
329	6	1.7	218	2	H70856	hypothetical prote
330	6	1.7	218	2	H82205	hypothetical prote
331	6	1.7	219	1	TVBYSR	transforming prote
332	6	1.7	219	2	G87221	transforming prote
333	6	1.7	219	2	T45545	hypothetical prote
334	6	1.7	219	2	T35105	probable two-compo
335	6	1.7	221	2	B84326	hypothetical prote
336	6	1.7	221	2	QXAS4M	NADH2 dehydrogenas
337	6	1.7	221	2	E64305	conserved hypothet
338	6	1.7	223	2	C71843	probable uroporphy
339	6	1.7	224	2	T28692	probable uroporphy
340	6	1.7	224	2	C86192	protein T20M3.4 (t
341	6	1.7	225	2	G75074	hypothetical prote
342	6	1.7	225	2	P71090	hypothetical prote
343	6	1.7	226	2	S57521	probable arsenical
344	6	1.7	226	2	AH2080	hypothetical prote
345	6	1.7	226	2	H64672	uroporphyrinogen I
346	6	1.7	227	2	T20104	hypothetical prote
347	6	1.7	228	2	F90626	ATP synthase F0 ch
348	6	1.7	228	2	AD2935	hypothetical prote
349	6	1.7	229	2	C87467	ABC transporter, A
350	6	1.7	230	2	JC7308	cellulase (EC 3.2.
351	6	1.7	230	2	S17399	torCAD operon tran
352	6	1.7	230	2	A64841	torCAD operon tran
353	6	1.7	230	2	B85635	response transcrip
354	6	1.7	230	2	C71864	response transcrip
355	6	1.7	230	1	P90772	response transcrip
356	6	1.7	231	2	S76832	hypothetical prote
357	6	1.7	231	2	A86644	hypothetical prote
358	6	1.7	231	2	E90887	late expression fa
359	6	1.7	232	2	T30473	cryptic nitrate re
360	6	1.7	232	2	D85730	cryptic nitrate re
361	6	1.7	232	2	S11429	nitrate reductase
362	6	1.7	233	2	S17399	Ig lambda chain Pr
363	6	1.7	234	2	I38667	agrobacterium viru
364	6	1.7	234	2	AE2456	hypothetical prote
365	6	1.7	234	2	AB3180	SNF8 protein - yea
366	6	1.7	236	2	A95852	melanoma antigen M
367	6	1.7	236	1	A95852	CD30 ligand - mous
368	6	1.7	239	2	S04742	fibroblast growth
369	6	1.7	239	2	B40710	conserved hypothet
370	6	1.7	239	2	B87280	hypothetical prote
371	6	1.7	239	2	G97165	protein-tyrosine k
372	6	1.7	241	2	PC4221	flagellar hook ass
373	6	1.7	241	2	AG1224	hlbA protein - Cor
374	6	1.7	241	2	AE0248	hypothetical prote
375	6	1.7	241	2	C83354	hypothetical prote
376	6	1.7	244	1	F96733	conserved hypothet
377	6	1.7	244	2	JE0213	MHC class II histo
378	6	1.7	244	2	J23100	arabinogalactan pr
379	6	1.7	245	2	C83354	integrase/recombin
380	6	1.7	245	2	I50127	recombinase, site
381	6	1.7	245	2	T48338	chloride conductan
382	6	1.7	246	2	AI1577	precorrin methylas
383	6	1.7	246	2	A53014	precorrin methylas
384	6	1.7	246	2	S48482	ubiquitin carrier
385	6	1.7	246	2	B98003	MADS box protein -
386	6	1.7	247	2	B42856	hypothetical prote
387	6	1.7	247	1	T23100	pulmonary surfacta
388	6	1.7	248	2	A48853	pulmonary surfacta
389	6	1.7	248	2	A48E53	conserved hypothet
390	6	1.7	248	2	A70044	tRNA/rRNA methyltr
391	6	1.7	249	2	B95334	probable transcrip
392	6	1.7	249	2	A83664	probable tRNA (gua
393	6	1.7	249	2	B83678	hypothetical prote
394	6	1.7	250	2	B37801	IstB protein homol

No.					Accession	Description
395	6	1.7	250	2	C64546	conserved hypothet
396	6	1.7	250	2	AE3261	hypothetical prote
397	6	1.7	250	2	D75343	conserved hypothet
398	6	1.7	250	2	I50126	MHC class II histo
399	6	1.7	252	2	G97851	hypothetical prote
400	6	1.7	253	2	D71975	hypothetical prote
401	6	1.7	253	2	E64532	hypothetical prote
402	6	1.7	253	2	A84278	hypothetical prote
403	6	1.7	253	2	AI2872	hypothetical prote
404	6	1.7	253	2	AF0521	pyruvate dehydroge
405	6	1.7	254	2	A97311	pyruvate dehydrog
406	6	1.7	255	2	T38115	uncharacterized pr
407	6	1.7	256	2	T50892	probable ATP-depen
408	6	1.7	256	2	T10586	spheroidene monoox
409	6	1.7	257	2	I40170	spheroidene monoox
410	6	1.7	257	2	I46080	small nuclear ribo
411	6	1.7	258	2	E81146	hypothetical prote
412	6	1.7	259	2	D95298	uroplakin Ia - bov
413	6	1.7	259	2	H86636	conserved hypothet
414	6	1.7	261	2	C84776	probable 4-carboxy
415	6	1.7	261	2	AI0053	chromosome partiti
416	6	1.7	261	2	AE1071	hypothetical prote
417	6	1.7	262	2	S56594	probable riboee 5-
418	6	1.7	262	2	G91294	hypothetical prote
419	6	1.7	262	2	B86136	hypothetical prote
420	6	1.7	262	2	H70953	tegument protein 6
421	6	1.7	263	2	T03162	hypothetical prote
422	6	1.7	263	2	I17302	hypothetical prote
423	6	1.7	265	2	T44414	probable ribosomal
424	6	1.7	265	2	H84422	probable methyltra
425	6	1.7	265	2	E87357	hypothetical prote
426	6	1.7	265	2	A83625	probable metalloen
427	6	1.7	265	2	C95885	ferric iron reduct
428	6	1.7	265	2	A64200	ferric iron reduct
429	6	1.7	267	2	JN0831	ferric iron reduct
430	6	1.7	268	2	F90142	ferrichrome-iron r
431	6	1.7	271	2	T41026	ferric iron reduct
432	6	1.7	271	2	T08009	probable ionic vol
433	6	1.7	271	2	T49956	DNA polymerase III
434	6	1.7	272	2	B72270	GlnR protein - Str
435	6	1.7	273	2	A71202	hypothetical prote
436	6	1.7	274	2	AF2025	conserved hypothet
437	6	1.7	274	2	G97034	probable L-isoaspa
438	6	1.7	275	2	D70737	hypothetical prote
439	6	1.7	275	2	F69402	probable metal-dep
440	6	1.7	276	2	T45275	conserved hypothet
441	6	1.7	276	2	D70191	oxidoreductase of
442	6	1.7	277	1	A45961	conserved hypothet
443	6	1.7	277	2	C70017	hypothetical prote
444	6	1.7	278	2	D47055	2,5-diketo-D-gluco
445	6	1.7	278	2	JH0124	4-hydroxybenzoyl-C
446	6	1.7	278	2	I51344	streptomycin resis
447	6	1.7	278	2	C83552	streptomycin resis
448	6	1.7	278	2	AG2176	dnaK-type molecula
449	6	1.7	279	2	F86842	hypothetical prote
450	6	1.7	279	2	A89920	prephenate dehydra
451	6	1.7	281	2	C69588	conserved hypothet
452	6	1.7	281	2	E75330	L-arabinose transp
453	6	1.7	281	2	B86896	degV protein - Dei
454	6	1.7	281	2	T03509	hypothetical prote
455	6	1.7	281	2	C97649	probable arsenate
456	6	1.7	283	2	H95194	probable ATP-bindi
457	6	1.7	283	2	E98061	conserved hypothet
458	6	1.7	284	2	D81199	conserved hypothet
459	6	1.7	284	2	D81834	conserved hypothet
460	6	1.7	284	2	AD3184	pirin-like protein
461	6	1.7	284	2	H83119	probable transcrip
462	6	1.7	284	2	T39544	suppressor protein
463	6	1.7	284	2	S27931	EnvZ/v-mpl fusion p
464	6	1.7	284	2	F82957	hypothetical prote
465	6	1.7	285	2	G97710	stage 0 sporulatio
466	6	1.7	286	2	F82082	transcription regu
467	6	1.7	287	2	S57770	xyloglucan endo-1,
468	6	1.7	287	2	T22324	hypothetical prote
469	6	1.7	287	2	T42085	MPT4 protein homol
470	6	1.7	288	2	H64453	conserved hypothet
471	6	1.7	289	2	B87708	hypothetical prote
472	6	1.7	289	2	S49812	glutamate racemase
473	6	1.7	290	2	AG2347	xyloglucan endo-1,
474	6	1.7	290	2	T18992	prephenate dehydra
475	6	1.7	290	1	T18706	hypothetical prote
476	6	1.7	291	2	P70463	hypothetical prote
477	6	1.7	291	2	F70463	methylenetetrahydr
478	6	1.7	292	1	T18706	hypothetical prote
479	6	1.7	293	2	A40644	transcription regu
480	6	1.7	293	1	A39871	calponin alpha, sm
481	6	1.7	294	2	A40587	transcription regu
482	6	1.7	295	2	JC5305	probable aminoacyl
483	6	1.7	295	2	A83055	hypothetical prote
484	6	1.7	295	2	D82658	probable transcrip
485	6	1.7	296	2	D69534	conserved hypothet
486	6	1.7	296	2	S31483	calponin H2 - pig
487	6	1.7	297	2	S31484	calponin H1 - rat
488	6	1.7	297	2	JN0773	calponin H1 - pig
489	6	1.7	297	2	S31486	hypothetical prote
490	6	1.7	297	1	S31486	calponin H1 - mous
491	6	1.7	297	2	I39495	basic calponin -.h
492	6	1.7	297	2	G02142	smooth muscle cell
493	6	1.7	297	2	C83285	hypothetical prote
494	6	1.7	298	2	H83863	probable transcrip
495	6	1.7	298	2	B35272	modulation of CheA
496	6	1.7	298	1	JC4130	hypothetical prote
497	6	1.7	299	2	A35272	osteoinductive fac
498	6	1.7	300	2	S41171	osteoglycin precur
499	6	1.7	300	1	AC0678	osteoinductive fac
500	6	1.7	300	2	I39495	transrepressor pro
501	6	1.7	300	2	A69351	probable membrane
502	6	1.7	301	2	S76574	heterodisulfide re
503	6	1.7	301	1	AB0164	heterodisulfide re
504	6	1.7	301	2	H71011	hypothetical prote
505	6	1.7	302	2	A70599	probable thiamin b
506	6	1.7	302	2	S27846	FecCD transport fa
507	6	1.7	303	2	D85356	hypothetical prote
508	6	1.7	304	2	D81445	ybiS protein precu
509	6	1.7	305	2	T13380	hypothetical prote
510	6	1.7	305	1	A31562	probable ABC trans
511	6	1.7	305	2	S31485	streptomycin 6-kin
512	6	1.7	305	2	T02851	probable permease
513	6	1.7	305	2	T49783	hypothetical prote
514	6	1.7	306	2	F82303	hypothetical prote
515	6	1.7	306	2	H90740	probable integral m
516	6	1.7	306	2	C64819	probable sulfotran
517	6	1.7	306	1	C85591	hypothetical prote
518	6	1.7	307	2	G95564	conserved hypothet
519	6	1.7	307	2	KISMCC	calponin - human
520	6	1.7	307	1	G97575	thiamin monophosph
521	6	1.7	308	2	AG2796	hypothetical prote
522	6	1.7	308	2	S76000	hypothetical prote
523	6	1.7	308	2	F70917	oligopeptide ABC t
524	6	1.7	309	2	C95935	hypothetical prote
525	6	1.7	310	2	P70917	hypothetical prote
526	6	1.7	310	2	JC4906	MLCL536.34 protein
527	6	1.7	311	2	H75153	hypothetical prote
528	6	1.7	311	2	C70871	conserved hypothet
529	6	1.7	311	1	H70792	hypothetical prote
530	6	1.7	312	2	A98304	protein W1OC8.1 [1
531	6	1.7	313	2	AD2979	hypothetical prote
532	6	1.7	313	2	T11017	conserved hypothet
533	6	1.7	313	2	A99933	conserved hypothet
534	6	1.7	315	2	A70708	cysteine synthase
535	6	1.7	315	2	S59448	olfactory receptor
536	6	1.7	316	2	H87731	R-phycoerythrin ga
537	6	1.7	316	2	B69397	hypothetical prote
538	6	1.7	317	2	F90589	hypothetical prote
539	6	1.7	317	2	F64182	hypothetical prote
540	6	1.7	318	2	A57069	hypothetical prote

#					Code	Description
541	6	1.7	318	2	G87342	hypothetical prote
542	6	1.7	319	2	S30173	probable mercuric
543	6	1.7	320	2	A95266	probable ABC trans
544	6	1.7	320	2	G95920	probable epimerase
545	6	1.7	321	2	G81404	UDP-3-O-[3-hydroxy
546	6	1.7	322	2	A83549	conserved hypothet
547	6	1.7	322	2	A97030	membrane protease
548	6	1.7	322	2	T12093	TGACG-motif bindin
549	6	1.7	322	2	C70700	hypothetical prote
550	6	1.7	322	2	T04595	hypothetical prote
551	6	1.7	322	2	E70326	conserved hypothet
552	6	1.7	323	2	D85526	probable permease
553	6	1.7	323	2	A99676	probable permease
554	6	1.7	323	2	E69177	conserved hypothet
555	6	1.7	323	2	A72508	probable cobalamin
556	6	1.7	323	1	QOBEB4	UL76 protein - hum
557	6	1.7	325	2	A69184	UDP-glucose 4-epim
558	6	1.7	325	2	H84230	transcription init
559	6	1.7	325	2	S59834	probable protein p
560	6	1.7	326	2	T08591	TGACG-motif bindin
561	6	1.7	326	2	A86411	protein F3M18.6 [i
562	6	1.7	326	2	AD2936	polymerase epsilon
563	6	1.7	326	2	C98346	hypothetical prote
564	6	1.7	327	2	T50744	spheroidene monoox
565	6	1.7	327	2	S49619	crtA protein - Rho
566	6	1.7	327	2	P83408	hypothetical prote
567	6	1.7	327	2	G96833	probable regulator
568	6	1.7	327	2	T34666	inhibin alpha-subu
569	6	1.7	328	2	S69715	hypothetical prote
570	6	1.7	328	2	G84826	probable phycoene
571	6	1.7	329	1	DWECTD	hypothetical prote
572	6	1.7	329	2	D85973	probable secreted
573	6	1.7	329	2	E91128	conserved hypothet
574	6	1.7	329	2	D69494	deacetoxycephalosp
575	6	1.7	329	2	JC4501	pyruvate formate-1
576	6	1.7	329	2	S32582	lipoprotein [impor
577	6	1.7	330	2	A53742	2-hydroxyglutaryl-
578	6	1.7	330	2	AH0697	acidic calponin -
579	6	1.7	330	2	S76408	structural protein
580	6	1.7	331	2	T35100	calponin, acidic -
581	6	1.7	331	2	T36969	probable secretion
582	6	1.7	331	2	E83368	hypothetical prote
583	6	1.7	331	2	A29711	probable secreted
584	6	1.7	332	2	H69494	conserved hypothet
585	6	1.7	332	2	AF0407	pyruvate formate-1
586	6	1.7	333	2	H83364	lipoprotein [impor
587	6	1.7	333	2	AD3261	hypothetical prote
588	6	1.7	334	2	A36707	cell division prot
589	6	1.7	334	2	F64674	protein-glutamate
590	6	1.7	334	2	A82206	aliphatic amidase
591	6	1.7	335	2	T45277	oligopeptide trans
592	6	1.7	335	2	C71842	Y box-binding prot
593	6	1.7	336	1	B38274	ABC transporter, A
594	6	1.7	336	2	A95213	hypothetical prote
595	6	1.7	336	2	B90077	ABC transport syst
596	6	1.7	336	1	P81348	alcohol dehydrogen
597	6	1.7	337	2	A42654	probable LPS biosy
598	6	1.7	337	2	F91191	probable LPS biosy
599	6	1.7	337	2	G86038	probable oxidoredu
600	6	1.7	337	2	AG0230	ribosomal large su
601	6	1.7	338	2	C75353	tagatose-1,6-dipho
602	6	1.7	338	2	AD1142	hypothetical prote
603	6	1.7	338	2	AD3052	hypothetical prote
604	6	1.7	338	2	H98233	hypothetical prote
605	6	1.7	339	2	D72509	hypothetical prote
606	6	1.7	340	1	WMBEL1	latency-related pr
607	6	1.7	340	2	T20101	hypothetical prote
608	6	1.7	340	2	E96019	hypothetical prote
609	6	1.7	341	2	E69544	probable sugar upt
610	6	1.7	341	2	D75479	hypothetical prote
611	6	1.7	341	2	F81276	probable sugar-pho
612	6	1.7	343	2	T36539	probable fructose
613	6	1.7	343	2	A49117	thromboxane A2 rec
614	6	1.7	343	2	A41748	lumican precursor
615	6	1.7	343	2	T26594	hypothetical proce
616	6	1.7	343	2	S03415	hypothetical prote
617	6	1.7	343	2	B86198	hypothetical prote
618	6	1.7	344	2	C82835	anthranilate phosp
619	6	1.7	344	2	T00110	integral membrane
620	6	1.7	345	2	T12359	NADH2 dehydrogenas
621	6	1.7	345	2	H72488	NADH2 dehydrogenas
622	6	1.7	345	2	S04280	peba intron 1 prot
623	6	1.7	345	2	A70664	probable anthranil
624	6	1.7	345	2	T35357	hypothetical prote
625	6	1.7	346	2	AG3399	plsX protein [impo
626	6	1.7	347	2	T45551	NADH2 dehydrogenas
627	6	1.7	347	2	T17074	NADH2 dehydrogenas
628	6	1.7	347	2	I38008	melanoma antigen M
629	6	1.7	348	2	D83554	hypothetical prote
630	6	1.7	348	2	AB3121	hypothetical prote
631	6	1.7	348	2	H95910	oxidoreductase moc
632	6	1.7	349	2	F69016	conserved hypothet
633	6	1.7	349	2	D70543	sensory transducti
634	6	1.7	349	2	S30143	probable nada prot
635	6	1.7	349	2	A39158	alternative respir
636	6	1.7	349	2	AD0990	alternative respir
637	6	1.7	349	2	AE2568	probable membrane
638	6	1.7	350	2	E87714	WD repeat protein
639	6	1.7	351	2	AE1923	hypothetical prote
640	6	1.7	352	2	AF3145	c-type cytochrome
641	6	1.7	352	2	E95885	hypothetical prote
642	6	1.7	353	2	B75400	probable iron ABC
643	6	1.7	353	2	T39599	phosphoribosylform
644	6	1.7	353	2	B91264	conserved hypothet
645	6	1.7	354	2	G86104	probable metabo
646	6	1.7	354	2	B65219	phosphonate metabo
647	6	1.7	354	2	T06748	phni protein - Esc
648	6	1.7	354	2	T51480	hypothetical prote
649	6	1.7	354	2	S19635	hypothetical prote
650	6	1.7	356	2	AB3650	probable zinc fing
651	6	1.7	356	2	E98142	hypothetical prote
652	6	1.7	356	2	T27338	hypothetical prote
653	6	1.7	356	2	T28084	tricarboxylate car
654	6	1.7	357	2	I55210	protein-glutamate
655	6	1.7	358	2	A82206	conserved hypothet
656	6	1.7	358	2	A75561	fructose 1,6-bisph
657	6	1.7	359	2	AC0875	hypothetical prote
658	6	1.7	359	2	E83262	hypothetical prote
659	6	1.7	359	2	T47187	hypothetical prote
660	6	1.7	359	1	D81317	inhibin alpha chai
661	6	1.7	360	2	A25732	probable glycosylt
662	6	1.7	360	2	T03373	inhibin alpha chai
663	6	1.7	360	1	E72467	probable G-box bin
664	6	1.7	361	2	T27504	probable non speci
665	6	1.7	361	2	B57737	hypothetical prote
666	6	1.7	361	2	A53860	phosphate carrier
667	6	1.7	361	1	T40857	chondroadherin pre
668	6	1.7	362	2	JQ0735	hypothetical prote
669	6	1.7	362	2	T26520	recF protein - Pro
670	6	1.7	362	2	A53737	hypothetical prote
671	6	1.7	362	2	B43680	phosphate carrier
672	6	1.7	362	2	B87571	K362 protein - Af
673	6	1.7	363	2	T16755	hypothetical prote
674	6	1.7	364	2	I45915	hypothetical prote
675	6	1.7	364	2	EDBESP	inhibin alpha chai
676	6	1.7	364	2	WFPGA	immediate-early pr
677	6	1.7	364	2	C86015	interstitial retin
678	6	1.7	364	2	F90672	hypothetical prote
679	6	1.7	364	1	T24657	probable adhesin [
686	6	1.7	364	2		hypothetical prote

ID					Accession	Description
687	6	1.7	365	2	A75375	hypothetical prote
688	6	1.7	366	1	A24248	inhibin alpha chai
689	6	1.7	366	1	A40056	inhibin alpha chai
690	6	1.7	366	1	JC1106	inhibin alpha chai
691	6	1.7	366	2	B41565	env polyprotein -
692	6	1.7	366	2	D83224	conserved hypothet
693	6	1.7	366	2	D75167	hypothetical prote
694	6	1.7	366	2	H86614	CT838 hypothetical
695	6	1.7	366	2	C72009	conserved hypothet
696	6	1.7	366	2	A75077	phnI protein [impo
697	6	1.7	367	2	C70820	iron (iii) abc tra
698	6	1.7	367	2	PB0401	probable alcohol de
699	6	1.7	367	2	T03828	hypothetical prote
700	6	1.7	368	2	AF1327	a NifS-like protei
701	6	1.7	368	2	E96023	myb protein - rice
702	6	1.7	368	2	T18184	probable C-P (carb
703	6	1.7	368	2	D83823	ankyrin repeat pro
704	6	1.7	369	2	A53959	two-component sens
705	6	1.7	369	2	B72327	thromboxane A-2 re
706	6	1.7	369	2	AE2598	dnaJ protein - The
707	6	1.7	369	2	F97380	conserved hypothet
708	6	1.7	369	2	G90757	phnI protein [impo
709	6	1.7	369	2	AG0625	conserved hypothet
710	6	1.7	369	2	B85523	hypothetical prote
711	6	1.7	369	2	B85621	hypothetical prote
712	6	1.7	370	2	B64835	probable iron-sulf
713	6	1.7	370	2	A69430	conserved hypothet
714	6	1.7	370	2	E83848	aminotransferase (
715	6	1.7	371	2	S77345	hypothetical prote
716	6	1.7	371	2	C83991	hypothetical prote
717	6	1.7	371	2	E72665	hypothetical prote
718	6	1.7	372	2	P97510	BA483f11.2.1 (cox1
719	6	1.7	373	2	A57559	3beta-hydroxy-Delt
720	6	1.7	373	2	JC4162	P2Y receptor - bov
721	6	1.7	373	2	JQ1648	SHL2 protein - hum
722	6	1.7	373	2	T47396	hypothetical prote
723	6	1.7	374	1	F70584	phosphate specific
724	6	1.7	375	2	S05390	fibromodulin precu
725	6	1.7	375	2	AH3110	oxoreductase [impo
726	6	1.7	375	2	D98176	hypothetical prote
727	6	1.7	376	1	KIBE17	thymidine kinase (
728	6	1.7	376	1	KIBET	thymidine kinase (
729	6	1.7	376	1	KIBE16	thymidine kinase (
730	6	1.7	376	1	KIBEHF	thymidine kinase (
731	6	1.7	376	1	KIBEKS	thymidine kinase (
732	6	1.7	376	1	KIBETC	thymidine kinase (
733	6	1.7	376	2	H90407	hypothetical prote
734	6	1.7	376	2	AC2189	polysaccharide pol
735	6	1.7	376	2	S55275	fibromodulin precu
736	6	1.7	376	2	JC5600	alpha-N-acetylneur
737	6	1.7	376	2	C91169	hypothetical prote
738	6	1.7	376	2	S47693	hypothetical 38.5K
739	6	1.7	379	2	T20972	hypothetical prote
740	6	1.7	379	2	B83677	phenylalanine dehy
741	6	1.7	379	2	B70937	hypothetical prote
742	6	1.7	379	2	T47507	probable protein k
743	6	1.7	380	2	S67857	GumH protein - Xan
744	6	1.7	380	2	S55275	cystathionine gamm
745	6	1.7	380	2	B64533	probable cystathio
746	6	1.7	380	2	D71973	factor VIII-associ
747	6	1.7	380	2	A42832	hypothetical prote
748	6	1.7	381	2	D82965	hypothetical prote
749	6	1.7	381	2	TVMVJ	transforming prote
750	6	1.7	381	2	B82653	phage-related prot
751	6	1.7	382	2	G84971	ompr-like porin [i
752	6	1.7	382	2	P96009	hypothetical membr
753	6	1.7	382	2	E83322	probable FAD-depen
754	6	1.7	383	2	G70946	probable dioxygena
755	6	1.7	383	2	T36080	hypothetical prote
756	6	1.7	383	2	E87680	probable NADH dehy
757	6	1.7	383	2	A72299	sugar isomerase -
758	6	1.7	384	2	T08970	hypothetical prote
759	6	1.7	384	2	G95950	probable ABC trans
	6	1.7	385	2	F72567	hypothetical prote

ID					Accession	Description
760	6	1.7	386	2	A70740	probable fadE14 pr
761	6	1.7	386	2	G71467	probable succinyl-
762	6	1.7	387	2	IS0703	transcription fact
763	6	1.7	387	2	S46123	hypothetical prote
764	6	1.7	388	2	A75321	preplin, peptidase
765	6	1.7	388	2	T50078	hypothetical prote
766	6	1.7	389	2	F72554	hypothetical prote
767	6	1.7	390	2	T35509	hypothetical prote
768	6	1.7	392	2	AD0420	phnI protein [impo
769	6	1.7	392	1	T19327	hypothetical prote
770	6	1.7	393	2	S42068	mitogen-activated
771	6	1.7	393	2	T33917	hypothetical prote
772	6	1.7	394	2	T25519	probable glutamate
773	6	1.7	394	1	B90007	similar to amidase
774	6	1.7	394	2	F72517	hypothetical prote
775	6	1.7	395	2	B71019	probable NADH-ubiq
776	6	1.7	395	2	AE3356	lipid-A-disacchari
777	6	1.7	396	2	B98166	moca protein [impo
778	6	1.7	396	2	A70581	hypothetical prote
779	6	1.7	397	2	S49301	AWJL175 protein -
780	6	1.7	397	2	A69135	bacteriochlorophyl
781	6	1.7	397	2	T36119	phnI protein [impo
782	6	1.7	397	2	AP2016	hypothetical prote
783	6	1.7	398	2	T05873	hypothetical prote
784	6	1.7	399	2	F72417	MFS permease [drug
785	6	1.7	399	2	AC2785	hypothetical prote
786	6	1.7	399	2	D97564	homoserine O-acety
787	6	1.7	401	2	G84392	hypothetical prote
788	6	1.7	401	2	S16738	porphobilinogen sy
789	6	1.7	401	2	C82660	conserved hypothet
790	6	1.7	402	1	I46053	connexin44 - bovin
791	6	1.7	404	2	T45026	glutamyl-tRNA redu
792	6	1.7	404	2	C71303	probable nitrogen
793	6	1.7	404	2	AD0032	probable type-III
794	6	1.7	405	2	AE3649	multidrug resistan
795	6	1.7	405	2	E72521	hypothetical prote
796	6	1.7	405	2	T43023	ceoA protein - Bur
797	6	1.7	406	2	C82660	hypothetical prote
798	6	1.7	406	2	AE2455	mRNA binding prote
799	6	1.7	406	2	I46053	hydroxyneurosporen
800	6	1.7	406	2	T48103	hypothetical prote
801	6	1.7	407	2	T50894	Na+/H+ exchange pr
802	6	1.7	407	2	B82686	probable thromboxa
803	6	1.7	407	2	T02670	endoglucanase B -
804	6	1.7	408	2	S12018	leucyl aminopeptid
805	6	1.7	409	2	JC5862	hypothetical prote
806	6	1.7	409	2	T19895	glucose-1-phosphat
807	6	1.7	412	2	E71369	probable spore coa
808	6	1.7	412	2	C72548	probable dihydroli
809	6	1.7	413	2	JC4862	activin beta-A cha
810	6	1.7	413	2	AG0632	glucose-1-phosphat
811	6	1.7	413	2	JV0087	glucose-1-phosphat
812	6	1.7	413	2	F90773	periplasmic glucos
813	6	1.7	413	2	B85636	periplasmic glucos
814	6	1.7	413	2	S65948	hemolin - cecropia
815	6	1.7	413	2	A37778	hemolin precursor
816	6	1.7	415	2	T12533	hypothetical prote
817	6	1.7	415	2	D75616	probable acyl-CoA
818	6	1.7	417	1	VGBEIB	glycoprotein D pre
819	6	1.7	417	2	S35784	glycoprotein gD -
820	6	1.7	417	2	TS1467	glucose 6 phosphat
821	6	1.7	417	2	AB1315	hypothetical prote
822	6	1.7	417	2	AB1687	hypothetical prote
823	6	1.7	417	2	AE2735	conserved hypothet
824	6	1.7	418	2	S62483	hypothetical prote
825	6	1.7	419	2	A25438	keratin, type I cy
826	6	1.7	419	2	G96002	hypothetical prote
827	6	1.7	421	2	F82279	probable sugar upt
828	6	1.7	422	2	F90250	D-amino acid dehyd
829	6	1.7	423	2	A55797	sugar phosphate nu
830	6	1.7	423	2	T31342	collagen precursor
831	6	1.7	423	2	A99242	ragD protein - Bra
832	6	1.7	423	2	AC3044	hypothetical prote

No.					ID	Description
833	6	1.7	424	1	B40905	inhibin beta-A cha
834	6	1.7	424	1	S31440	inhibin beta-A cha
835	6	1.7	424	1	WFPGBA	inhibin beta-A cha
836	6	1.7	424	2	B81960	probable inner mem
837	6	1.7	424	2	C70651	hypothetical prote
838	6	1.7	425	1	S50898	hypothetical prote
839	6	1.7	425	1	AC3391	tetracenomycin c p
840	6	1.7	425	2	147072	inhibin beta-A cha
841	6	1.7	425	2	G83969	cell-division prot
842	6	1.7	425	2	S60446	hypothetical prote
843	6	1.7	425	2	T12473	hypothetical prote
844	6	1.7	425	2	B97516	hypothetical prote
845	6	1.7	426	1	B24248	inhibin beta-A cha
846	6	1.7	426	1	T51506	hypothetical prote
847	6	1.7	426	2	A82660	glucose/galactose
848	6	1.7	426	2	A30212	alpha-factor recep
849	6	1.7	426	2	C41903	glutamate-1-semial
850	6	1.7	427	2	S57898	glutamate-1-semial
851	6	1.7	427	2	G83149	tetrahydrofolylpol
852	6	1.7	427	2	B86769	ArB protein PA227
853	6	1.7	427	2	G83361	glycosyltransferas
854	6	1.7	427	2	AD3149	hypothetical prote
855	6	1.7	427	2	G98138	hypothetical prote
856	6	1.7	429	2	A83807	arsenical pump mem
857	6	1.7	429	1	B25937	arsenical pump mem
858	6	1.7	429	1	B41902	arsenical pump mem
859	6	1.7	429	1	F91175	arsenical pump mem
860	6	1.7	429	2	F86021	arsenical pump mem
861	6	1.7	429	2	AE0406	arsenical pump mem
862	6	1.7	430	2	G89962	hypothetical prote
863	6	1.7	430	2	C90696	probable amino aci
864	6	1.7	430	2	G85546	probable amino aci
865	6	1.7	430	2	E64779	probable membrane
866	6	1.7	430	2	T45437	hypothetical prote
867	6	1.7	430	2	A81237	arsenic efflux pum
868	6	1.7	431	2	AD1237	arsenic efflux pum
869	6	1.7	431	2	AI1599	conserved hypothet
870	6	1.7	432	1	E70373	ToiB protein PA097
871	6	1.7	432	2	P83525	probable ABC trans
872	6	1.7	432	2	C95275	keratin, type I, e
873	6	1.7	433	2	S01631	deoxyguanosinetrip
874	6	1.7	435	2	D75352	arsenical pump mem
875	6	1.7	435	2	G69779	hypothetical prote
876	6	1.7	436	2	T46443	cartilage-derived
877	6	1.7	436	2	B54452	arsenic efflux pum
878	6	1.7	436	2	G84024	arsenite efflux pu
879	6	1.7	436	2	S47723	conserved hypothet
880	6	1.7	437	2	H84865	probable sterol de
881	6	1.7	438	2	T45602	glucosyltransferas
882	6	1.7	438	2	B84919	Nct56-like protein
883	6	1.7	439	2	H70582	probable transposa
884	6	1.7	439	2	B86302	hypothetical prote
885	6	1.7	439	2	S51378	probable membrane
886	6	1.7	439	2	G97159	contains cell adhe
887	6	1.7	440	1	S60755	rhodopsin - Allote
888	6	1.7	441	2	S14441	retinol-binding pr
889	6	1.7	441	2	CB3318	conserved hypothet
890	6	1.7	441	2	T23461	hypothetical prote
891	6	1.7	442	2	A71486	nitrile hydratase
892	6	1.7	442	2	B82633	probable yop N (fl
893	6	1.7	442	2	T38691	hypothetical prote
894	6	1.7	442	2	D87351	conserved hypothet
895	6	1.7	442	2	S50062	cell wall glycopro
896	6	1.7	444	2	C81054	phosphoglucomutase
897	6	1.7	444	2	C81823	probable phosphogl
898	6	1.7	444	2	B95065	conserved hypothet
899	6	1.7	444	2	P97932	conserved hypothet
900	6	1.7	444	2	S48696	suppressor protein
901	6	1.7	445	2	T24723	hypothetical prote
902	6	1.7	446	2	G81326	probable DNA repai
903	6	1.7	446	2	T51368	sterile apetala [v
904	6	1.7	447	2	T12978	hypothetical prote
905	6	1.7	448	2	AE2590	two component resp
906	6	1.7	448	2	A81369	probable lipoprote
907	6	1.7	449	2	T45605	glucosyltransferas
908	6	1.7	449	2	AD3181	two component sens
909	6	1.7	449	2	H70652	hypothetical prote
910	6	1.7	450	2	T31188	hypothetical prote
911	6	1.7	450	2	T40337	probable saccharop
912	6	1.7	450	2	C86262	F13K23.12 protein
913	6	1.7	451	2	B81056	proteinase, probab
914	6	1.7	451	2	C81820	proteinase, probab
915	6	1.7	451	2	H75593	probable proteinas
916	6	1.7	452	1	S14332	rhodopsin - northe
917	6	1.7	453	1	T37054	hypothetical prote
918	6	1.7	454	2	T35016	probable 3-carboxy
919	6	1.7	454	2	T70448	signal recognition
920	6	1.7	454	2	T02275	hypothetical prote
921	6	1.7	454	2	G75105	hypothetical prote
922	6	1.7	455	1	JC4338	tryptophan dimethy
923	6	1.7	455	2	T31440	UDP-N-acetylmuramy
924	6	1.7	455	2	H71028	hypothetical prote
925	6	1.7	456	2	F97372	probable two-compo
926	6	1.7	456	2	C86624	hypothetical prote
927	6	1.7	456	2	H72000	hypothetical prote
928	6	1.7	457	2	H85059	phosphomannomutase
929	6	1.7	457	2	AF3426	probable sugar tra
930	6	1.7	458	2	E71059	probable endo-1,4-
931	6	1.7	459	2	JC2057	chromosomal replic
932	6	1.7	459	2	AC2057	anthranilate N-hyd
933	6	1.7	461	2	D89894	hypothetical prote
934	6	1.7	462	2	AC0672	hypothetical prote
935	6	1.7	462	2	S11431	nitrite extrusion
936	6	1.7	462	2	A85730	nitrite extrusion
937	6	1.7	462	2	S11431	nitrite extrusion
938	6	1.7	463	2	H90887	nitrite extrusion
939	6	1.7	463	2	T09243	dnaK-type molecula
940	6	1.7	464	2	C82967	dnaK-type molecula
941	6	1.7	465	2	T07620	probable peptidase
942	6	1.7	465	2	JC5184	probable endo-1,4-
943	6	1.7	466	2	E70865	glutamate synthase
944	6	1.7	467	2	I50476	trigger factor tig
945	6	1.7	467	2	S21172	keratin type I - g
946	6	1.7	468	2	T45475	heat-shock protein
947	6	1.7	468	2	T45476	glutamate-tRNA lig
948	6	1.7	468	2	H70427	heat-shock protein
949	6	1.7	469	2	G82329	replicative DNA he
950	6	1.7	469	2	T45478	replicative DNA he
951	6	1.7	470	2	T34645	heat-shock protein
952	6	1.7	470	2	S36536	transcription regu
953	6	1.7	470	2	E70085	hypothetical prote
954	6	1.7	471	2	F96806	probable AUX1-like
955	6	1.7	471	2	B97433	transcription regu
956	6	1.7	471	2	AC2651	hypothetical prote
957	6	1.7	471	2	T21972	hypothetical prote
958	6	1.7	472	2	S76290	ribulose-biphosph
959	6	1.7	472	2	A31082	ribulose-biphosph
960	6	1.7	473	2	T27754	hypothetical prote
961	6	1.7	473	2	C64371	hypothetical prote
962	6	1.7	473	2	H72419	L2 protein - human
963	6	1.7	475	2	T19707	L2 protein
964	6	1.7	475	2	C71404	transmembrane tran
965	6	1.7	475	2	C96503	transmembrane tran
966	6	1.7	475	2	D64799	virulence factor M
967	6	1.7	475	2	A85565	aspartate kinase (
968	6	1.7	476	2	D90714	protein F9C16.7 [1
969	6	1.7	476	2	T26850	protein F9C16.7 [1
970	6	1.7	477	2	S09152	ybeS protein - Esc
971	6	1.7	477	2	H66619	hypothetical prote
972	6	1.7	477	2	G72003	probable enzyme of
973	6	1.7	478	2	H83389	probable enzyme of
974	6	1.7	478	2	S47040	hypothetical prote
975	6	1.7	479	2	H83590	hypothetical prote
976	6	1.7	479	2	T23508	translation elonga
977	6	1.7	479	2	G95092	shikimate 5-dehydr
978	6	1.7	480	2	P72205	3-dehydroquinate d
979	6	1.7	480	2	JC7866	hypothetical prote
980	6	1.7	480	2		gene Tts2 protein

#					Accession	Description
979	6	1.7	482	2	G75483	probable leucyl am
980	6	1.7	482	2	JH0310	arginine/ornithine
981	6	1.7	483	2	E84596	AUX1-like amino ac
982	6	1.7	485	2	S03834	hypothetical prote
983	6	1.7	486	2	T51431	glucosyltransferas
983	6	1.7	487	2	B83095	UDP-N-acetylmuramo
984	6	1.7	487	2	AE0488	probable membrane
985	6	1.7	488	1	QXA5M4	probable membrane
986	6	1.7	488	2	QXA5M4	NADH2 dehydrogenas
986	6	1.7	488	2	D70876	probable polyketid
987	6	1.7	488	2	C75488	argininosuccinate
988	6	1.7	488	2	A27253	collagen alpha 1(I
988	6	1.7	488	2	C41977	histamine H1 recep
989	6	1.7	488	2	I56507	retinoid receptor
990	6	1.7	490	2	T23791	LAX1 / AUX1-like p
991	6	1.7	490	2	T45964	hypothetical prote
991	6	1.7	492	2	A81852	3',5'-cyclic-nucle
992	6	1.7	492	2	A40283	probable type III
993	6	1.7	493	2	F84689	probable cytochrom
993	6	1.7	493	2	G84689	probable cytochrom
996	6	1.7	493	2	T10054	pyruvate kinase (E
997	6	1.7	493	2	I49370	plasma phospholipi
998	6	1.7	493	2	T48934	acyl CoA reductase

ALIGNMENTS

RESULT 1
JC5241
activin beta E chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
A;Accession: JC5241; JC5367
R;Fang, J.; Yin, W.; Smiley, E.; Wang, S.Q.; Bonadio, J.
Biochem. Biophys. Res. Commun. 228, 669-674, 1996
A;Title: Molecular cloning of the mouse activin beta E subunit gene.
A;Reference number: JC5241; MUID:97095313; PMID:8941337
A;Contents: liver
A;Accession: JC5241
A;Molecule type: mRNA
A;Residues: 1-350 <FAN>
A;Cross-references: UNIPROT:O08717; GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g20725
C;Genetics:
A;Cross-references: GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522
A;Introns: 99/3
C;Superfamily: inhibin

Query Match   19.1%; Score 67; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 8.6e-58;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   244  TPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLK  303
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   244  TPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLK  303

Qy   304  ANNPWPA  310
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Db   304  ANNPWPA  310
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RESULT 2
JC2466
inhibin beta-C chain precursor - human
N;Alternate names: activin beta C chain
C;Species: Homo sapiens (man)
C;Date: 29-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JC2466
R;Hoetten, G.; Neidhardt, H.; Schneider, C.; Pohl, J.
Biochem. Biophys. Res. Commun. 206, 608-613, 1995
A;Title: Cloning of a new member of the TGF-beta family: A putative new activin betaC c...
A;Reference number: JC2466; MUID:95126961; PMID:7826378
A;Accession: JC2466
A;Molecule type: mRNA
A;Residues: 1-352 <HOE>
A;Cross-references: UNIPROT:P55103; GB:X82540; NID:g669154; PIDN:CAA57890.1; PID:g66915
C;Genetics:
A;Experimental source: liver
C;Genetics: GDB:INHBC
A;Cross-references: GDB:632884
A;Map position: 2cen-2q13
C;Superfamily: inhibin
A;Keywords: glycoprotein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-236/Domain: propeptide #status predicted <PRO>
F;237-352/Product: activin beta C #status predicted <MAT>
F;110,143,161/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   4.3%; Score 15; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   313  SCCVPTARRPLSLLY  327
          |||||||||||||||
Db   315  SCCVPTARRPLSLLY  329
```

RESULT 3
S70580
activin beta C precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
A;Accession: S70580
R;Lau, A.L.; Nishimori, K.; Matzuk, M.M.
Biochim. Biophys. Acta 1307, 145-148, 1996
A;Title: Structural analysis of the mouse activin beta-C gene.
A;Reference number: S70580; MUID:96283807; PMID:8679697
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <LAU>
A;Cross-references: UNIPROT:P55104; EMBL:U40772
C;Genetics:
A;Introns: 106/1
C;Superfamily: inhibin

Query Match   3.1%; Score 11; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   340  PDMVVEACGCS  350
          |||||||||||
Db   342  PDMVVEACGCS  352
```

RESULT 4
JC5366
activin beta C - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
A;Accession: JC5366
R;Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.
Biochem. Biophys. Res. Commun. 231, 655-661, 1997
A;Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibi
A;Reference number: JC5366; MUID:97224404; PMID:9070865
A;Molecule type: DNA
A;Residues: 1-352 <FAN>
A;Accession: JC5366
A;Cross-references: UNIPROT:P55104; GB:U95962
C;Comment: Activin beta C and beta E form a distinct subset of related activins.

RESULT 5
S43296

Query Match 3.1%; Score 11; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 340 PDMVVEACGCS 350
         |||||||||||
Db 342 PDMVVEACGCS 352

C;Genetics:
A;Introns: 105/3
C;Superfamily: inhibin

C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1994 #sequence_revision 09-Jul-2004
C;Accession: S43296
R;Storm, E. E.; Huynh, T. V.; Copeland, N. G.; Jenkins, N. A.; Kingsley, D. M.; Lee, S. J.
Nature 368, 639-643, 1994
A;Title: Limb alterations in brachypodism mice due to mutations in a new member of the T
A;Reference number: S43294; MUID:94195427; PMID:8145850
A;Accession: S43296
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-151 <STO>
A;Cross-references: UNIPROT:P43029; GB:U08339; NID:g488465; PIDN:AAA18780.1; PID:g488466
C;Superfamily: inhibin
bone morphogenetic protein-related protein (GDF7) - mouse

RESULT 6
T14455

Query Match 2.6%; Score 9; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 341 DMVVEACGC 349
         |||||||||
Db 142 DMVVEACGC 150

C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14455
R;Croy, R. R. D.; Booker, J. P.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z18098
A;Accession: T14455
A;Molecule type: mRNA
A;Residues: 1-283 <CRO>
A;Cross-references: UNIPROT:Q39374; EMBL:Z74841; NID:e1001204; PID:e256042
A;Experimental source: strain alboglabra; stigma
A;Status: preliminary; translated from GB/EMBL/DDBJ
hypothetical protein - wild cabbage (fragment)

RESULT 7
D86425

Query Match 2.3%; Score 8; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 KIRANEPG 229
         ||||||||
Db 193 KIRANEPG 200

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86425
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
unknown protein [imported] - Arabidopsis thaliana

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucas, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S. L.; Schwartz, J. R.; Shinn, P.; Southwick, A. M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: D86425
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-311 <STO>
A;Cross-references: UNIPROT:Q9C6Z4; GB:AE005172; NID:g11094785; PIDN:AAG29717.1; GSPDB:
A;Genetics:
A;Map position: 1

RESULT 8
JC4151

Query Match 2.3%; Score 8; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 KIRANEPG 229
         ||||||||
Db 175 KIRANEPG 182

C;Species: Xenopus laevis (African clawed frog)
C;Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: JC4151
R;Oda, S.; Nishimatsu, S.; Murakami, K.; Ueno, N.
Biochem. Biophys. Res. Commun. 210, 581-588, 1995
A;Title: Molecular cloning and functional analysis of a new activin beta subunit: a dor
A;Reference number: JC4151; MUID:95275314; PMID:7755637
A;Accession: JC4151
A;Molecule type: mRNA
A;Residues: 1-367 <ODA>
A;Cross-references: UNIPROT:Q91696; DDBJ:D49543; NID:g961512; PIDN:BAA08494.1; PID:g961
A;Superfamily: inhibin
A;Experimental source: embryo
A;Keywords: glycoprotein; mesoderm
C;Superfamily: inhibin
C;Species: Xenopus laevis (African clawed frog)
activin beta D chain precursor - African clawed frog

RESULT 9
S22701

Query Match 2.3%; Score 8; DB 2; Length 367;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 45 ELAKQQIL 52
        ||||||||
Db 47 ELAKQQIL 54

C;Species: Saccharomyces cerevisiae
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S22701; S64040
R;Nakayama, K.I.; Nagasu, T.; Shimma, Y.; Kuromitsu, J.; Jigami, Y.
EMBO J. 11, 2511-2519, 1992
A;Title: OCH1 encodes a novel membrane bound mannosyltransferase: outer chain elongatio
A;Reference number: S22701; MUID:92331603; PMID:1628616
A;Accession: S22701
A;Molecule type: DNA
A;Residues: 1-480 <NAK>
A;Cross-references: UNIPROT:P31755; EMBL:D11095; NID:g218450; PIDN:BAA01869.1; PID:g218.
R;Hebling, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64003
N;Alternate names: protein G3626; protein YGL038c
F;j-253/Domain: signal sequence #status predicted <SIG>
F;254-367/Product: activin beta D chain #status predicted <MAT>
F;64,155,161,208,230/Binding site: carbohydrate (Asn) (covalent) #status predicted
mannosyltransferase (EC 2.4.1.-) - yeast (Saccharomyces cerevisiae)

A;Accesion: S6040
A;Molecule type: DNA
A;Residues: 1-480 <HEB>
A;Cross-references: EMBL:Z72560; NID:e243938; PID:g1322519; PID:g1322520; MIPS:YGL038c
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:OCH1
A;Cross-references: SGD:S0003006; MIPS:YGL038c
A;Map position: 7L
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase; transmembrane protein
F;16-32/Domain: transmembrane #status predicted <TMM>
F;203,281,341,393/Binding site: carbohydrate (Asn) (covalent) #status predicted

```
Qy  107 SLLTFHLS 114
        ||||||||
Db   26 SLLTFHLS 33
```

Query Match   2.3%;   Score 8;   DB 2;   Length 480;
Best Local Similarity   100.0%;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 10
A29840
serine proteinase (EC 3.4.21.-) precursor - Serratia marcescens (strain IFO-3046)
C;Species: Serratia marcescens
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C;Accession: A29840
R;Yanagida, N.; Uozumi, T.; Beppu, T.
J;Bacteriol.166, 937-944, 1986
A;Title: Specific excretion of Serratia marcescens protease through the outer membrane o
A;Reference number: A29840
A;Accession: A29840; MUID:86223815; PMID:3011754
A;Molecule type: DNA
A;Residues: 1-1045 <YAN>
A;Cross-references: UNIPROT:P09489; GB:M13469; NID:g152857; PIDN:AAA26572.1; PID:g152858
A;Superfamily: autotransporter subtilisin-like protease precursor; subtilisin homology
C;Keywords: hydrolase; serine proteinase
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-408/Product: serine proteinase #status predicted <MAT>
F;67-355/Domain: subtilisin homology <SBT>
F;409-1045/Domain: carboxyl-terminal propeptide #status predicted <PRO>
F;76,112,341/Active site: Asp, His, Ser #status predicted

```
Qy   82 GSVAPGNG 89
        ||||||||
Db  525 GSVAPGNG 532
```

Query Match   2.3%;   Score 8;   DB 2;   Length 1045;
Best Local Similarity   100.0%;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 11
S63993
acrosomal protein Azl - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C;Accession: S63993
R;Aoto, H.; Tsuchida, J.; Nishimune, Y.; Asano, A.; Tajima, S.
submitted to the EMBL Data Library, December 1994
A;Description: Isolation of a novel cDNA that encodes a protein localized to the pre-acr
A;Reference number: S63993
A;Accession: S63993
A;Molecule type: mRNA
A;Residues: 1-1060 <AOT>
A;Cross-references: UNIPROT:Q62036; EMBL:D43921; NID:g1827501; PIDN:BAA07868.1; PID:d100
C;Note: this is a revision to the sequence from reference S63992
R;Aoto, H.; Tsuchida, J.; Nishina, Y.; Nishimune, Y.; Asano, A.; Tajima, S.
Eur. J. Biochem. 234, 8-15, 1995
A;Title: Isolation of a novel cDNA that encodes a protein localized to the pre-acrosome
A;Reference number: S63992; MUID:96096715; PMID:8529672
A;Accession: S63992

A;Molecule type: mRNA
A;Residues: 1-942, 'SGCSP' <AOW>
A;Cross-references: EMBL:D43921
A;Note: this sequence has been revised in reference S63993

```
Qy   70 AALTRALR 77
        ||||||||
Db  807 AALTRALR 814
```

Query Match   2.3%;   Score 8;   DB 2;   Length 1060;
Best Local Similarity   100.0%;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 12
E72611
probable ATP-dependent DNA helicase APE1353 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: E72611
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
A;Reference number: A72450; MUID:99310339; PMID:10382266
A;Accession: E72611
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1273 <KAW>
A;Cross-references: UNIPROT:Q9YCA1; DDBJ:AP000061; NID:g5104821; PIDN:BAA80347.1; PID:d
C;Genetics:
A;Experimental source: strain K1
A;Gene: APE1353

```
Qy  176 SGLRGEKS 183
        ||||||||
Db 1121 SGLRGEKS 1128
```

Query Match   2.3%;   Score 8;   DB 2;   Length 1273;
Best Local Similarity   100.0%;
Matches   8;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 13
S28793
major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragment)
N;Alternate names: major surface antigen p190
C;Species: Plasmodium falciparum
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S28793
R;Hall, R.; Hyde, J.E.; Goman, M.; Simmons, D.L.; Hope, I.A.; Mackay, M.; Scaife, J.; M
Nature 311, 379-382, 1984
A;Title: Major surface antigen gene of a human malaria parasite cloned and expressed in
A;Reference number: S28793; MUID:85012680; PMID:6089934
A;Accession: S28793
A;Molecule type: mRNA
A;Residues: 1-72 <HAL>
A;Cross-references: UNIPROT:Q25925; EMBL:M32152; NID:g160423; PIDN:AAA29658.1; PID:g160
C;Superfamily: major merozoite surface antigen
C;Keywords: merozoite; surface antigen

```
Qy  221 LKIRANE 227
        |||||||
Db   26 LKIRANE 32
```

Query Match   2.0%;   Score 7;   DB 2;   Length 72;
Best Local Similarity   100.0%;
Matches   7;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

RESULT 14
G84229
hypothetical protein Vng0724h [imported] - Halobacterium sp. NRC-1

```
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84229
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84229
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <STO>
A;Cross-references: UNIPROT:Q9HRF5; GB:AE004437; NID:g10580303; PIDN:AAG19203.1; GSPDB:G
C;Genetics:
A;Gene: VNG0724H

Qy       319 ARRPLSL 325
             |||||||
Db        12 ARRPLSL 18

     Query Match          2.0%;    Score 7;  DB 2;  Length 86;
     Best Local Similarity  100.0%;  Pred. No. 36;
     Matches   7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;


RESULT 15
AH3212
hypothetical protein Atu5431 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AH3212
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel1
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AH3212
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <KUR>
A;Cross-references: UNIPROT:Q8UP5; GB:AE008687; PIDN:AAL46118.1; PID:g17743884; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5431
A;Genome: plasmid

     Query Match          2.0%;    Score 7;  DB 2;  Length 129;
     Best Local Similarity  100.0%;  Pred. No. 51;
     Matches   7;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy       155 RTLLAEH 161
             |||||||
Db        24 RTLLAEH 30


Search completed: October 13, 2005, 18:47:17
Job time : 80 secs
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OM protein - protein search, using sw model

```
                     GenCore version 5.1.6
                     Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:              October 13, 2005, 18:38:45 ; Search time 43 Seconds
                                                  (without alignments)
                                                  607.609 Million cell updates/sec

Title:               US-10-666-225-14
Perfect score:       350
Sequence:            1 MRLPDVQLMLVILWALVRAQ.........NGNVVKTDVPDMVVEACGCS 350

Scoring table:       Gapop 60.0 , Gapext 60.0
Searched:            513545 seqs, 74649064 residues
Word size :          6

Total number of hits satisfying chosen parameters:       2107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :           Issued_Patents_AA:*
             1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
             2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
             3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
             4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
             5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

             Pred. No. is the number of results predicted by chance to have a
             score greater than or equal to the score of the result being printed,
             and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	350	100.0	350	2	US-08-765-662-14	Sequence 14, Appl
2	350	100.0	350	5	PCT-US95-08745-14	Sequence 14, Appl
3	119	34.0	119	2	US-08-274-215A-12	Sequence 12, Appl
4	119	34.0	119	2	US-08-765-662-12	Sequence 12, Appl
5	119	34.0	119	5	US-09-184-933-12	Sequence 12, Appl
6	119	34.0	119	5	PCT-US95-08745-12	Sequence 12, Appl
7	119	34.0	119	1	US-08-482-577B-24	Sequence 24, Appl
8	106	4.3	106	1	US-08-289-222E-28	Sequence 28, Appl
9	106	4.3	106	3	US-09-218-176-7	Sequence 7, Appli
10	106	4.3	106	3	US-09-054-526B-28	Sequence 28, Appl
11	106	4.3	106	3	US-08-482-577B-2	Sequence 2, Appli
12	35	4.3	352	3	US-08-289-222E-4.	Sequence 4, Appli
13	352	3.1	352	3	US-09-218-176-2	Sequence 2, Appli
14	352	3.1	352	3	US-09-054-526B-4	Sequence 4, Appli
15	352	3.1	352	3	US-08-289-222E-4	Sequence 4, Appli
16	352	3.1	352	1	US-08-981-490B-3	Sequence 3, Appli
17	35	3.1	352	1	US-09-374-958C-23	Sequence 23, Appl
18	352	3.1	352	4	US-08-482-577B-4	Sequence 4, Appli
19	352	3.1	352	4	US-09-218-176-2	Sequence 2, Appli
20	13	2.6	352	4	US-09-374-958C-74	Sequence 74, Appl
21	35	2.6	35	4	US-09-374-958C-17	Sequence 17, Appl
22	35	2.6	35	4	US-09-374-958C-34	Sequence 34, Appl
23	102	2.6	102	4	US-09-374-958C-87	Sequence 87, Appl
24	102	2.6	102	4	US-09-374-958C-88	Sequence 88, Appl
25	117	2.6	117	4	US-09-374-958C-69	Sequence 69, Appl
26	119	2.6	119	2	US-08-581-528A-7	Sequence 7, Appli
27	119	2.6	119	4	US-09-412-791D-7	Sequence 7, Appli
28	9	2.6	119	5	PCT-US94-07799-7	Sequence 7, Appli
29	9	2.6	129	1	US-08-360-914B-15	Sequence 15, Appl
30	9	2.6	129	1	US-08-741-589A-13	Sequence 13, Appl
31	9	2.6	139	2	US-09-374-958C-68	Sequence 68, Appl
32	9	2.6	140	4	US-09-374-958C-90	Sequence 90, Appl
33	9	2.6	160	4	US-09-252-991A-17039	Sequence 17039, A
34	9	2.6	161	2	US-09-412-791D-6	Sequence 6, Appl
35	9	2.6	161	5	US-09-581-528A-6	Sequence 6, Appli
36	9	2.6	161	6	PCT-US94-07799-6	Sequence 6, Appli
37	9	2.6	240	1	US-08-333-576C-30	Sequence 30, Appl
38	9	2.6	240	3	US-08-363-670B-30	Sequence 30, Appl
39	9	2.6	240	3	US-08-808-324-30	Sequence 30, Appl
40	9	2.6	240	5	US-09-945-182-30	Sequence 30, Appl
41	9	2.6	294	5	PCT-US94-14030A-30	Sequence 30, Appl
42	9	2.6	294	3	US-08-362-670B-2	Sequence 2, Appli
43	9	2.6	294	1	US-08-333-576C-2	Sequence 2, Appli
44	9	2.6	294	3	US-08-808-324-2	Sequence 2, Appli
45	9	2.6	294	5	US-09-945-182-2	Sequence 2, Appli
46	9	2.6	294	5	PCT-US94-14030A-2	Sequence 2, Appli
47	9	2.6	388	1	US-08-362-670B-34	Sequence 34, Appl
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319	6	1.7	77	3	US-08-052-888-21	Sequence 21, Appl

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320	6	1.7	77	4	US-09-723-890-21	Sequence 21, Appl
321	6	1.7	77	4	US-09-723-901-21	Sequence 21, Appl
322	6	1.7	77	4	US-09-723-547-21	Sequence 21, Appl
323	6	1.7	77	4	US-09-724-127-21	Sequence 21, Appl
324	6	1.7	77	4	US-09-723-931-21	Sequence 21, Appl
325	6	1.7	77	4	US-09-723-873-21	Sequence 21, Appl
326	6	1.7	77	4	US-09-724-114-21	Sequence 21, Appl
327	6	1.7	77	4	US-09-723-913-21	Sequence 21, Appl
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330	6	1.7	77	4	US-09-724-157-21	Sequence 21, Appl
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332	6	1.7	77	4	US-09-724-065-21	Sequence 21, Appl
333	6	1.7	77	4	US-09-270-767-57875	Sequence 57875, A
334	6	1.7	78	4	US-09-489-039A-8935	Sequence 8935, Ap
335	6	1.7	80	4	US-09-270-767-39725	Sequence 39725, A
336	6	1.7	80	4	US-09-270-767-54942	Sequence 54942, A
337	6	1.7	82	4	US-09-248-796A-24266	Sequence 24266, A
338	6	1.7	83	4	US-09-248-796A-26013	Sequence 26013, A
339	6	1.7	83	4	US-09-902-540-12932	Sequence 12932, A
340	6	1.7	84	4	US-09-107-532A-5281	Sequence 5281, Ap
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342	6	1.7	88	3	US-09-513-999C-7338	Sequence 7338, Ap
343	6	1.7	89	3	US-09-270-767-60514	Sequence 60514, A
344	6	1.7	91	3	US-09-690-454-75	Sequence 75, Appl
345	6	1.7	92	5	US-07-807-529A-2	Sequence 2, Appl
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354	6	1.7	95	3	US-08-431-184-11	Sequence 11, Appl
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385	6	1.7	98	3	US-08-513-999C-6080	Sequence 6080, Ap
386	6	1.7	99	3	US-08-931-858E-170	Sequence 170, App
387	6	1.7	99	3	US-08-981-739-170	Sequence 170, App
388	6	1.7	99	3	US-09-128-026-170	Sequence 170, App
389	6	1.7	99	4	US-09-220-616-170	Sequence 170, App
390	6	1.7	99	4	US-09-220-527-170	Sequence 170, App
391	6	1.7	99	4	US-09-220-407-170	Sequence 170, App
392	6	1.7	102	4	US-09-374-958C-84	Sequence 84, Appl

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397	6	1.7	105	4	US-08-478-097A-22	Sequence 22, Appl
398	6	1.7	105	4	US-08-289-222E-31	Sequence 31, Appl
399	6	1.7	105	3	US-09-218-176-10	Sequence 10, Appl
400	6	1.7	105	4	US-09-054-526B-31	Sequence 31, Appl
401	6	1.7	105	3	US-08-931-858E-169	Sequence 169, Appl
402	6	1.7	105	3	US-09-001-472-2	Sequence 2, Appli
403	6	1.7	105	3	US-08-981-739-169	Sequence 169, App
404	6	1.7	105	4	US-09-128-026-169	Sequence 169, App
405	6	1.7	105	4	US-09-071-035-292	Sequence 292, App
406	6	1.7	105	4	US-08-857-389-26	Sequence 26, Appl
407	6	1.7	105	4	US-09-496-398-22	Sequence 22, Appl
408	6	1.7	105	4	US-09-775-827A-2	Sequence 2, Appli
409	6	1.7	105	4	US-09-775-827A-13	Sequence 13, Appl
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414	6	1.7	105	3	US-09-374-958C-61	Sequence 61, Appl
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416	6	1.7	105	4	US-09-220-407-169	Sequence 169, Appl
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424	6	1.7	106	4	US-09-220-527-153	Sequence 153, App
425	6	1.7	106	4	US-09-128-026-153	Sequence 153, App
426	6	1.7	106	4	US-09-378-238-36	Sequence 36, Appl
427	6	1.7	106	4	US-09-496-398-23	Sequence 23, Appl
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433	6	1.7	106	4	US-09-220-527-153	Sequence 153, App
434	6	1.7	106	4	US-09-220-407-153	Sequence 153, App
435	6	1.7	107	4	US-09-252-991A-32005	Sequence 32005, A
436	6	1.7	107	4	US-09-489-039A-7336	Sequence 7336, Appl
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439	6	1.7	109	4	US-09-374-958C-63	Sequence 63, Appl
440	6	1.7	110	4	US-09-271-252-4	Sequence 4, Appli
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454	6	1.7	116	1	US-08-459-850-35	Sequence 35, Appl
455	6	1.7	116	1	US-08-459-850-38	Sequence 38, Appl
456	6	1.7	116	1	US-08-459-214-35	Sequence 35, Appl
457	6	1.7	116	1	US-08-459-214-38	Sequence 38, Appl
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462	6	1.7	116	3	US-08-581-528A-15	Sequence 15, Appl
463	6	1.7	116	3	US-09-097-616-15	Sequence 15, Appl
464	6	1.7	116	3	US-09-177-860A-25	Sequence 25, Appl
465	6	1.7	116	3	US-08-624-635-17	Sequence 17, Appl
					US-09-145-060-21	Sequence 21, Appl

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467	6	1.7	116	4	US-09-629-938-25	Sequence 25, Appl
468	6	1.7	116	4	US-09-686-344-43	Sequence 43, Appl1
469	6	1.7	116	4	US-09-412-791D-15	Sequence 15, Appl1
470	6	1.7	116	4	US-09-619-061-15	Sequence 15, Appl1
471	6	1.7	116	5	PCT-US94-00657-21	Sequence 21, Appl1
472	6	1.7	116	5	PCT-US94-07762-15	Sequence 15, Appl
473	6	1.7	116	5	PCT-US94-07799-15	Sequence 15, Appl
474	6	1.7	116	6	5206160-1	Patent No. 5206160
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476	6	1.7	116	2	US-08-249-013-6	Sequence 6, Appl1
477	6	1.7	117	2	US-08-886-863-6	Sequence 6, Appl1
478	6	1.7	117	1	US-09-175-229-6	Sequence 6, Appl1
479	6	1.7	117	5	PCT-US95-06764-6	Sequence 6, Appl1
480	6	1.7	118	3	US-09-199-637A-279	Sequence 279, App
481	6	1.7	118	4	US-09-252-991A-21453	Sequence 21453, .
482	6	1.7	118	4	US-09-619-061-7	Sequence 7, Appl1
483	6	1.7	119	1	US-09-270-767-56640	Sequence 56640, A
484	6	1.7	119	2	US-08-460-402-11	Sequence 11, Appl1
485	6	1.7	119	1	US-09-153-733A-21	Sequence 21, Appl1
486	6	1.7	119	4	US-08-946-092A-18	Sequence 18, Appl1
487	6	1.7	119	4	US-09-619-061-9	Sequence 9, Appl1
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490	6	1.7	119	5	PCT-US94-07762-7	Sequence 7, Appl1
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492	6	1.7	120	4	US-09-134-000C-4898	Sequence 4898, Ap
493	6	1.7	121	3	US-08-481-377-20	Sequence 20, Appl
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497	6	1.7	121	3	US-09-153-733A-20	Sequence 20, Appl
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499	6	1.7	121	3	US-09-389-705-20	Sequence 20, Appl
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516	6	1.7	122	2	US-08-455-559-23	Sequence 23, Appl
517	6	1.7	122	2	US-09-097-616-16	Sequence 16, Appl
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520	6	1.7	122	3	US-09-177-860A-27	Sequence 27, Appl
521	6	1.7	122	2	US-08-624-635-18	Sequence 18, Appl
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529	6	1.7	122	3	US-09-412-791D-16	Sequence 16, Appl
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535	6	1.7	122	4	US-09-619-061-16	Sequence 16, Appl
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543	6	1.7	122	5	PCT-US94-07799-16	Sequence 16, Appl
544	6	1.7	122	5	PCT-US94-07799-17	Sequence 17, Appl
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546	6	1.7	124	4	US-09-270-767-32001	Sequence 32001, A
547	6	1.7	124	4	US-09-270-767-47218	Sequence 47218, A
548	6	1.7	124	4	US-09-893-737-48	Sequence 48, Appl
549	6	1.7	127	4	US-09-270-767-37348	Sequence 37348, A
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551	6	1.7	129	4	US-09-949-016-8110	Sequence 8110, Ap
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554	6	1.7	130	1	US-09-570-923-21	Sequence 21, Appl
555	6	1.7	130	1	US-09-580-014-21	Sequence 21, Appl
556	6	1.7	130	3	US-09-252-991A-19533	Sequence 19533, A
557	6	1.7	130	4	US-09-628-126-21	Sequence 21, Appl
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562	6	1.7	131	4	US-09-902-540-11259	Sequence 11259, A
563	6	1.7	131	4	US-10-170-097-654	Sequence 654, App
564	6	1.7	132	4	US-09-621-976-4084	Sequence 4084, Ap
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ALIGNMENTS

RESULT 1

US-08-765-662-14
Patent No. 592213
Sequence 14, Application US/08765662
GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,662
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08745
; FILING DATE: 12-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/042WO1 (PD-3830)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-765-662-14

Query Match 100.0%; Score 350; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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Sequence 14, Application PC/TUS950745
GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08745
; FILING DATE: 12-JUL-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/042WO1 (PD-3830)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

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; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
PCT-US95-08745-14

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RESULT 3
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; Sequence 12, Application US/08274215A
; Patent No. 5831054
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Esquela, Aurora F.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/274,215A
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/040001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-68-5099
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-274-215A-12

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; Sequence 12, Application US/08765662
; Patent No. 5929213
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
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; APPLICATION NUMBER: US/08/765,662
; FILING DATE: 28-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08745
; FILING DATE: 12-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/042W01 (PD-3830)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
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US-08-765-662-12

Query Match             34.0%;  Score 119;  DB 2;  Length 119;
Best Local Similarity   100.0%;  Pred. No. 2.1e-108;
Matches 119;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  232 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 291
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIA 60
```

RESULT 5
US-09-184-933-12
Sequence 12, Application US/09184933
Patent No. 6130050
GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: Esquela, Aurora F.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/274,215
; FILING DATE: 13-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/040001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-68-5099
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-184-933-12

Query Match   34.0%; Score 119; DB 3; Length 119;
Best Local Similarity   100.0%; Pred. No. 2.1e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   232 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWIIQPEGYQLNYCSGQCPPHLAGSPGIA 291
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWIIQPEGYQLNYCSGQCPPHLAGSPGIA 60

Qy   292 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119

RESULT 6
PCT-US95-08745-12
Sequence 12, Application PC/TUS950874S
GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08745
; FILING DATE: 12-JUL-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
PCT-US95-08745-12

Query Match   34.0%; Score 119; DB 5; Length 119;
Best Local Similarity   100.0%; Pred. No. 2.1e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   232 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWIIQPEGYQLNYCSGQCPPHLAGSPGIA 291
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 RARRRTPTCEPATPLCCRRDHYVDFQELGWRDWIIQPEGYQLNYCSGQCPPHLAGSPGIA 60

Qy   292 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 350
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ASFHSAVFSLLKANNPWPASTSCCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS 119

RESULT 7
US-08-482-577B-24
Sequence 24, Application US/08482577B
Patent No. 5807713
GENERAL INFORMATION:
; APPLICANT: HOTTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM
; STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
; STREET: SUITE 330
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08,482,577B

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
    NAME: KLESNER, SHARON
    REGISTRATION NUMBER: 36,335
    REFERENCE/DOCKET NUMBER: P564-5010
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 202/638-5000
    TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 24:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 106 amino acids
        TYPE: amino acid
        STRANDEDNESS: single
        TOPOLOGY: linear
    MOLECULE TYPE: peptide
US-08-482-577B-24

Qy   313 SCCVPTARRPLSLLY 327
         |||||||||||||||
Db   69 SCCVPTARRPLSLLY 83

Query Match
Best Local Similarity   100.0%;   Score 15;   DB 1;   Length 106;
Matches 15; Conservative 0; Pred. No. 9.7e-07; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
US-08-289-222E-28
Sequence 28, Application US/0828922E
Patent No. 6120760
GENERAL INFORMATION:
    APPLICANT: HOTTEN, GERTRUD
    APPLICANT: NEIDHARDT, HELGE
    APPLICANT: BECHTOLD, ROLF
    APPLICANT: POHL, JENS
    TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
    NUMBER OF SEQUENCES: 53
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM
        STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
        STREET: SUITE 330
        CITY: WASHINGTON
        STATE: DC
        COUNTRY: USA
        ZIP: 20005-5701
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: Patentin Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/08/289,222E
        FILING DATE: 25-AUG-1999
        CLASSIFICATION: 424
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/289,222
        FILING DATE: 12-AUG-1994
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: DE P 44 23 190.3
        FILING DATE: 07-JUL-1994
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: EPO 92102324.8
        FILING DATE: 12-FEB-1992
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/EP93/00350
        FILING DATE: 12-FEB-1993
    ATTORNEY/AGENT INFORMATION:
        NAME: KITTS, MONICA CHIN
        REGISTRATION NUMBER: 36,105
        REFERENCE/DOCKET NUMBER: P564-9021
    TELECOMMUNICATION INFORMATION:

    TELEPHONE: 202/638-5000
    TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 28:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 106 amino acids
        TYPE: amino acid
        STRANDEDNESS:
        TOPOLOGY: linear
    MOLECULE TYPE: protein
US-08-289-222E-28

Qy   313 SCCVPTARRPLSLLY 327
         |||||||||||||||
Db   69 SCCVPTARRPLSLLY 83

Query Match
Best Local Similarity   100.0%;   Score 15;   DB 3;   Length 106;
Matches 15; Conservative 0; Pred. No. 9.7e-07; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
US-09-218-176-7
Sequence 7, Application US/09218176
Patent No. 6171584
GENERAL INFORMATION:
    APPLICANT: H TTEN, Gertrud
    APPLICANT: NEIDHARDT, Helge
    APPLICANT: BECHTOLD, Rolf
    APPLICANT: POHL, Jens
    APPLICANT: PAULISTA, Michael
    TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
    TITLE OF INVENTION: TGF- FAMILY
    NUMBER OF SEQUENCES: 49
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
        STREET: 655 Fifteenth Street, N. W., G Street Lobby,
        STREET: Suite 330
        CITY: Washington
        STATE: DC
        COUNTRY: USA
        ZIP: 20005
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: IBM PC compatible
        OPERATING SYSTEM: PC-DOS/MS-DOS
        SOFTWARE: Patentin Release #1.0, Version #1.30
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/218,176
        FILING DATE: Herewith
        CLASSIFICATION:
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 08/679,048
        FILING DATE: 12-JUL-1996
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/482,577
        FILING DATE: 7-JUN-1995
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/EP93/00350
        FILING DATE: 2-FEB-1993
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: PCT/EP96/03065
        FILING DATE: 12-JUL-1996
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: EP 92 102 324.8
        FILING DATE: 12-FEB-1992
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: DE P 44 23 190.3
        FILING DATE: 01-JUL-1994
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: DE 195 11 243.1
        FILING DATE: 27-MAR-1995
    ATTORNEY/AGENT INFORMATION:

```
NAME: KITTS, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202/638-5000
  TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 7:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  106 amino acids
    TYPE: amino acid
    STRANDEDNESS:
    TOPOLOGY: linear
    MOLECULE TYPE: protein
US-09-218-176-7
```

```
Qy    313 SCCVPTARRPLSLLY 327
              |||||||||||||||
Db     69 SCCVPTARRPLSLLY 83
```

```
Query Match       4.3%;   Score 15;  DB 3;  Length 106;
Best Local Similarity  100.0%;   Pred. No. 9.7e-07;
Matches  15;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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```
RESULT 10
US-09-054-526B-28
Sequence 28, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
  APPLICANT: H TTEN, GERTRUD
  APPLICANT: NEIDHARDT, HELGE
  APPLICANT: BECHTOLD, ROLF
  APPLICANT: POHL, JENS
  TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
  TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
  NUMBER OF SEQUENCES: 53
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
    STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
    STREET: SUITE 330
    CITY: WASHINGTON
    STATE: DC
    COUNTRY: USA
    ZIP: 20005-5701
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/054,526B
    FILING DATE: 03-APR-1998
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/289,222
    FILING DATE: 12-AUG-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US/09/054,526B
    FILING DATE: 01-JUL-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: DE P 44 23.190.3
    FILING DATE: 01-JUL-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: EPO 92102324.8
    FILING DATE: 12-FEB-1992
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/EP93/00350
    FILING DATE: 12-FEB-1993
  ATTORNEY/AGENT INFORMATION:
    NAME: KITTS, MONICA CHIN
    REGISTRATION NUMBER: 36,105
    REFERENCE/DOCKET NUMBER: P564-8005
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 202/638-5000
    TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 28:
  SEQUENCE CHARACTERISTICS:
```

```
    LENGTH:  106 amino acids
    TYPE: amino acid
    STRANDEDNESS:
    TOPOLOGY: linear
    MOLECULE TYPE: protein
US-09-054-526B-28
```

```
Qy    313 SCCVPTARRPLSLLY 327
              |||||||||||||||
Db     69 SCCVPTARRPLSLLY 83
```

```
Query Match       4.3%;   Score 15;  DB 3;  Length 106;
Best Local Similarity  100.0%;   Pred. No. 9.7e-07;
Matches  15;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
RESULT 11
US-08-482-577B-2
Sequence 2, Application US/08482577B
Patent No. 5807713
GENERAL INFORMATION:
  APPLICANT: HOTTEN, GERTRUD
  APPLICANT: NEIDHARDT, HELGE
  APPLICANT: BECHTOLD, ROLF
  APPLICANT: POHL, JENS
  TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
  TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
  NUMBER OF SEQUENCES: 49
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM
    STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
    STREET: SUITE 330
    CITY: WASHINGTON
    STATE: DC
    COUNTRY: USA
    ZIP: 20005
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/482,577B
    FILING DATE:
    CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: KLESNER, SHARON
    REGISTRATION NUMBER: 36,335
    REFERENCE/DOCKET NUMBER: P564-5010
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 202/638-5000
    TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 2:
  SEQUENCE CHARACTERISTICS:
    LENGTH:  352 amino acids
    TYPE: amino acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: peptide
US-08-482-577B-2
```

```
Qy    313 SCCVPTARRPLSLLY 327
              |||||||||||||||
Db    315 SCCVPTARRPLSLLY 329
```

```
Query Match       4.3%;   Score 15;  DB 1;  Length 352;
Best Local Similarity  100.0%;   Pred. No. 3e-06;
Matches  15;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
RESULT 12
US-08-289-222E-4
Sequence 4, Application US/08289222E
```

Patent No. 6120760
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-4810
TELEFAX: 202/638-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-289-222E-4

Query Match 4.3%; Score 15; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   313 SCCVPTARRPLSLLY 327
         |||||||||||||||
Db   315 SCCVPTARRPLSLLY 329
```

RESULT 13
US-09-218-176-2
Sequence 2, Application US/09218176
Patent No. 6171584
GENERAL INFORMATION:
APPLICANT: H TIEN, Gertrud
APPLICANT: NEIDHARDT, Helge
APPLICANT: BECHTOLD, Rolf
APPLICANT: POHL, Jens
APPLICANT: PAULISTA, Michael

TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
TITLE OF INVENTION: TGF- FAMILY
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., G Street Lobby,
STREET: Suite 330
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,176
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/03065
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/679,048
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,577
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 11 243.1
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, Monica Chin
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-218-176-2

Query Match 4.3%; Score 15; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   313 SCCVPTARRPLSLLY 327
         |||||||||||||||
Db   315 SCCVPTARRPLSLLY 329
```

RESULT 14
US-09-054-526B-4
Sequence 4, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H TIEN, GERTRUD

```
;   APPLICANT: NEIDHARDT, HELGE
;   APPLICANT: BECHTOLD, ROLF
;   APPLICANT: POHL, JENS
;   TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
;   TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS
;   NUMBER OF SEQUENCES: 53
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
;   STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
;   STREET: SUITE 330
;   CITY: WASHINGTON
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20005-5701
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/054,526B
;   FILING DATE: 03-APR-1998
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/289,222
;   FILING DATE: 12-AUG-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: DE P 44 23 190.3
;   FILING DATE: 01-JUL-1994
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: EPO 92102324.8
;   FILING DATE: 12-FEB-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/EP93/00350
;   FILING DATE: 12-FEB-1993
;   ATTORNEY/AGENT INFORMATION:
;   NAME: KITTS, MONICA CHIN
;   REGISTRATION NUMBER: 36,105
;   REFERENCE/DOCKET NUMBER: P564-8005
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202/638-5000
;   TELEFAX: 202/638-4810
;   INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 352 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-054-526B-4

Query Match             4.3%;   Score 15;   DB 3;   Length 352;
Best Local Similarity  100.0%;   Pred. No. 3e-06;
Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      313 SCCVPTARPLSLLY 327
            ||||||||||||||
Db      315 SCCVPTARPLSLLY 329


RESULT 15
US-08-981-490B-3
Sequence 3, Application US/08981490B
Patent No. 6531450
;   GENERAL INFORMATION:
;   APPLICANT: Hotten, Gertrud
;   APPLICANT: Pohl, Jens
;   APPLICANT: Bechtold, Rolf
;   APPLICANT: Paulista, Michael
;   APPLICANT: Unsicker, Klaus
;   TITLE OF INVENTION: USE OF MP52 OR MP121 FOR TREATING AND PREVENTING DISEASES OF THE
;   TITLE OF INVENTION: NERVOUS SYSTEM
;   FILE REFERENCE: 100564-07032
;   CURRENT APPLICATION NUMBER: US/08/981,490B
```

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;   CURRENT FILING DATE: 1998-05-18
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;   SOFTWARE: Patentin version 3.1
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